



SEQUENCE LISTING

<110> Yaffe, Michael B.
Elia, Andrew E.H.
Rellos, Peter
Cantley, Lewis C.
Smerdon, Stephen J.
Manke, Isaac

<120> Computer Comprising Atomic Coordinates of a PLK-1 Polo-Box Domain
and Uses Thereof

<130> 01997/545003

<140> US 10/713,978
<141> 2003-11-14

<150> US 60/487,899
<151> 2003-07-17

<150> US 60/485,641
<151> 2003-07-08

<150> US 60/426,132
<151> 2002-11-14

<160> 129

<170> PatentIn version 3.3

<210> 1
<211> 603
<212> PRT
<213> Homo sapien

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Pro Gly Lys Ala Gly Val Pro Gly Val Ala Ala Pro Gly Ala Pro Ala
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Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
35 40 45

Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
50 55 60

Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
65 70 75 80

Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
 85 90 95

Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
 100 105 110

Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
 115 120 125

Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg
 130 135 140

Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
 145 150 155 160

Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
 165 170 175

Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
 180 185 190

Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys
 195 200 205

Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Ser
 210 215 220

Lys Lys Gly His Ser Phe Glu Val Asp Val Trp Ser Ile Gly Cys Ile
 225 230 235 240

Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser Cys Leu
 245 250 255

Lys Glu Thr Tyr Leu Arg Ile Lys Lys Asn Glu Tyr Ser Ile Pro Lys
 260 265 270

His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr
 275 280 285

Asp Pro Thr Ala Arg Pro Thr Ile Asn Glu Leu Leu Asn Asp Glu Phe
 290 295 300

Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr

305		310		315		320
Ile Pro Pro Arg Phe Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Asn						
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Arg Lys Pro Leu Thr Val Leu Asn Lys Gly Leu Glu Asn Pro Leu Pro						
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Glu Arg Pro Arg Glu Lys Glu Glu Pro Val Val Arg Glu Thr Gly Glu						
	355		360		365	
Val Val Asp Cys His Leu Ser Asp Met Leu Gln Gln Leu His Ser Val						
	370		375		380	
Asn Ala Ser Lys Pro Ser Glu Arg Gly Leu Val Arg Gln Glu Glu Ala						
	385		390		395	400
Glu Asp Pro Ala Cys Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp						
	405		410		415	
Tyr Ser Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val						
	420		425		430	
Gly Val Leu Phe Asn Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly						
	435		440		445	
Asp Ser Leu Gln Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr						
	450		455		460	
Val Ser Ser His Pro Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Lys						
	465		470		475	480
Tyr Phe Arg Asn Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn						
	485		490		495	
Ile Thr Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg						
	500		505		510	
Thr Trp Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly						
	515		520		525	
Ser Val Gln Ile Asn Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys						
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Xaa Xaa Xaa Xaa Ser Xaa Xaa
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<211> 15

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<220>

<221> MOD_RES

<222> (8)..(8)

<223> PHOSPHORYLATION

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<210> 4

<211> 685

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
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Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
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Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
 115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 180 185 190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
 195 200 205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
 210 215 220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
 225 230 235 240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
 245 250 255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
 260 265 270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
 275 280 285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
 290 295 300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
 305 310 315 320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

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Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro		
340	345	350
Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala		
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Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr		
370	375	380
His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His		
385	390	395
Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr		
405	410	415
Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr		
420	425	430
Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile		
435	440	445
Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu		
450	455	460
Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg		
465	470	475
Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln		
485	490	495
Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn		
500	505	510
Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu		
515	520	525
Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val		
530	535	540
His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp		
545	550	555
		560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
660 665 670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
675 680 685

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<211> 646
<212> PRT
<213> Homo sapiens

<400> 5

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Leu Arg Gly Pro Glu Leu Glu Met Leu Ala Gly Leu Pro Thr Ser Asp
35 40 45

Pro Gly Arg Leu Ile Thr Asp Pro Arg Ser Gly Arg Thr Tyr Leu Lys
50 55 60

Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr Glu Ala Thr
 65 70 75 80

Asp Thr Glu Thr Gly Ser Ala Tyr Ala Val Lys Val Ile Pro Gln Ser
 85 90 95

Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Leu Asn Glu Ile Glu
 100 105 110

Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe Ser His His
 115 120 125

Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu Cys Ser Arg
 130 135 140

Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu Leu Glu Pro
 145 150 155 160

Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu Lys Tyr Leu
 165 170 175

His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly Asn Phe Phe
 180 185 190

Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly Leu Ala Ala
 195 200 205

Arg Leu Glu Pro Pro Glu Gln Arg Lys Lys Thr Ile Cys Gly Thr Pro
 210 215 220

Asn Tyr Val Ala Pro Glu Val Leu Leu Arg Gln Gly His Gly Pro Glu
 225 230 235 240

Ala Asp Val Trp Ser Leu Gly Cys Val Met Tyr Thr Leu Leu Cys Gly
 245 250 255

Ser Pro Pro Phe Glu Thr Ala Asp Leu Lys Glu Thr Tyr Arg Cys Ile
 260 265 270

Lys Gln Val His Tyr Thr Leu Pro Ala Ser Leu Ser Leu Pro Ala Arg
 275 280 285

Gln Leu Leu Ala Ala Ile Leu Arg Ala Ser Pro Arg Asp Arg Pro Ser

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Ile Asp Gln Ile Leu Arg His Asp Phe Phe Thr Lys Gly Tyr Thr Pro				
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Asp Arg Leu Pro Ile Ser Ser Cys Val Thr Val Pro Asp Leu Thr Pro				
	325		330	335
Pro Asn Pro Ala Arg Ser Leu Phe Ala Lys Val Thr Lys Ser Leu Phe				
	340		345	350
Gly Arg Lys Lys Lys Ser Lys Asn His Ala Gln Glu Arg Asp Glu Val				
	355		360	365
Ser Gly Leu Val Ser Gly Leu Met Arg Thr Ser Val Gly His Gln Asp				
	370		375	380
Ala Arg Pro Glu Ala Pro Ala Ala Ser Gly Pro Ala Pro Val Ser Leu				
	385		390	395 400
Val Glu Thr Ala Pro Glu Asp Ser Ser Pro Arg Gly Thr Leu Ala Ser				
	405		410	415
Ser Gly Asp Gly Phe Glu Glu Gly Leu Thr Val Ala Thr Val Val Glu				
	420		425	430
Ser Ala Leu Cys Ala Leu Arg Asn Cys Ile Ala Phe Met Pro Pro Ala				
	435		440	445
Glu Gln Asn Pro Ala Pro Leu Ala Gln Pro Glu Pro Leu Val Trp Val				
	450		455	460
Ser Lys Trp Val Asp Tyr Ser Asn Lys Phe Gly Phe Gly Tyr Gln Leu				
	465		470	475 480
Ser Ser Arg Arg Val Ala Val Leu Phe Asn Asp Gly Thr His Met Ala				
	485		490	495
Leu Ser Ala Asn Arg Lys Thr Val His Tyr Asn Pro Thr Ser Thr Lys				
	500		505	510
His Phe Ser Phe Ser Val Gly Ala Val Pro Arg Ala Leu Gln Pro Gln				
	515		520	525

Leu Gly Ile Leu Arg Tyr Phe Ala Ser Tyr Met Glu Gln His Leu Met
530 535 540

Lys Gly Gly Asp Leu Pro Ser Val Glu Glu Val Glu Val Pro Ala Pro
545 550 555 560

Pro Leu Leu Leu Gln Trp Val Lys Thr Asp Gln Ala Leu Leu Met Leu
565 570 575

Phe Ser Asp Gly Thr Val Gln Val Asn Phe Tyr Gly Asp His Thr Lys
580 585 590

Leu Ile Leu Ser Gly Trp Glu Pro Leu Leu Val Thr Phe Val Ala Arg
595 600 605

Asn Arg Ser Ala Cys Thr Tyr Leu Ala Ser His Leu Arg Gln Leu Gly
610 615 620

Cys Ser Pro Asp Leu Arg Gln Arg Leu Arg Tyr Ala Leu Arg Leu Leu
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Arg Asp Arg Ser Pro Ala
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<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MOD_RES
<222> (5)..(5)
<223> PHOSPHORYLATION

<400> 6

Pro Met Gln Ser Thr Pro Leu
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<210> 7
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = Met, Tyr, Phe, Ile, Leu, His, or Lys

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa = Ala, His, Met, Thr, Phe, or Gln

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = Ser, Ala, Gly, or Thr

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa = Phosphorylated Serine or Phosphorylated Threonine

<400> 7

Xaa Xaa Xaa Xaa

1

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = Any amino acid

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa = Met, Tyr, Phe, Ile, Leu, His, or Lys

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = Ala, His, Met, Thr, Phe, or Gln

<220>

<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Ser, Ala, Gly, or Thr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = phosphorylated Ser or phosphorylated Thr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Pro, Met, or Asn

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = any amino acid

<400> 8

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = phosphorylated Threonine or phosphorylated Serine

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Met Gln Ser Xaa Pro Leu
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<210> 10
<211> 9
<212> PRT
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<223> synthetic

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<222> (4)..(4)

<223> Xaa = phosphorylated Ser or phosphorylated Thr

<400> 10

Tyr Asp Ile Xaa Gln Val Phe Pro Phe

1

5

<210> 11

<211> 82899

<212> DNA

<213> Homo sapiens

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			20					25					30		

Glu	Pro	Val	Ser	Thr	Lys	Cys	Asp	His	Ile	Phe	Cys	Lys	Phe	Cys	Met	35	40	45	
Leu	Lys	Leu	Leu	Asn	Gln	Lys	Lys	Gly	Pro	Ser	Gln	Cys	Pro	Leu	Cys	50	55	60	
Lys	Asn	Asp	Ile	Thr	Lys	Arg	Ser	Leu	Gln	Glu	Ser	Thr	Arg	Phe	Ser	65	70	75	80
Gln	Leu	Val	Glu	Glu	Leu	Leu	Lys	Ile	Ile	Cys	Ala	Phe	Gln	Leu	Asp	85	90	95	
Thr	Gly	Leu	Glu	Tyr	Ala	Asn	Ser	Tyr	Asn	Phe	Ala	Lys	Lys	Glu	Asn	100	105	110	
Asn	Ser	Pro	Glu	His	Leu	Lys	Asp	Glu	Val	Ser	Ile	Ile	Gln	Ser	Met	115	120	125	
Gly	Tyr	Arg	Asn	Arg	Ala	Lys	Arg	Leu	Leu	Gln	Ser	Glu	Pro	Glu	Asn	130	135	140	
Pro	Ser	Leu	Gln	Glu	Thr	Ser	Leu	Ser	Val	Gln	Leu	Ser	Asn	Leu	Gly	145	150	155	160
Thr	Val	Arg	Thr	Leu	Arg	Thr	Lys	Gln	Arg	Ile	Gln	Pro	Gln	Lys	Thr	165	170	175	
Ser	Val	Tyr	Ile	Glu	Leu	Gly	Ser	Asp	Ser	Ser	Glu	Asp	Thr	Val	Asn	180	185	190	
Lys	Ala	Thr	Tyr	Cys	Ser	Val	Gly	Asp	Gln	Glu	Leu	Leu	Gln	Ile	Thr	195	200	205	
Pro	Gln	Gly	Thr	Arg	Asp	Glu	Ile	Ser	Leu	Asp	Ser	Ala	Lys	Lys	Ala	210	215	220	
Ala	Cys	Glu	Phe	Ser	Glu	Thr	Asp	Val	Thr	Asn	Thr	Glu	His	His	Gln	225	230	235	240
Pro	Ser	Asn	Asn	Asp	Leu	Asn	Thr	Thr	Glu	Lys	Arg	Ala	Ala	Glu	Arg	245	250	255	

His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu
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Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser
 275 280 285

Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
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Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
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Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
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Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
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Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu
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Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp
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Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
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Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu
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Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
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Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr
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Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn
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Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg

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His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr		
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Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln		
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Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp		
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Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys		
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Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser		
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Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys		
595	600	605
Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu		
610	615	620
Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln		
625	630	635
Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn		
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Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys		
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Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr		
675	680	685
Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn		
690	695	700
Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu		
705	710	715
		720

Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu
 725 730 735

Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu
 740 745 750

Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser
 755 760 765

Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser
 770 775 780

Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys
 785 790 795 800

Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His
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Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro
 820 825 830

Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu
 835 840 845

Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser
 850 855 860

Lys Arg Gln Ser Phe Ala Pro Phe Ser Asn Pro Gly Asn Ala Glu Glu
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Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser
 885 890 895

Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys
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 915 920 925

Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys
 930 935 940

Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly
 945 950 955 960

Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn
 965 970 975

Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr
 980 985 990

Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met
 995 1000 1005

Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val
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Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Glu
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Ala Ser Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu
 1040 1045 1050

Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile
 1055 1060 1065

Gln Ala Glu Leu Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met
 1070 1075 1080

Leu Arg Leu Gly Val Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu
 1085 1090 1095

Pro Gly Ser Asn Cys Lys His Pro Glu Ile Lys Lys Gln Glu Tyr
 1100 1105 1110

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 1115 1120 1125

Ile Ser Asp Asn Leu Glu Gln Pro Met Gly Ser Ser His Ala Ser
 1130 1135 1140

Gln Val Cys Ser Glu Thr Pro Asp Asp Leu Leu Asp Asp Gly Glu
 1145 1150 1155

Ile Lys	Glu Asp Thr Ser Phe	Ala Glu Asn Asp Ile	Lys Glu Ser
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Ser Ala	Val Phe Ser Lys Ser	Val Gln Lys Gly Glu	Leu Ser Arg
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Ser Pro	Ser Pro Phe Thr His	Thr His Leu Ala Gln	Gly Tyr Arg
1190	1195	1200	
Arg Gly	Ala Lys Lys Leu Glu	Ser Ser Glu Glu Asn	Leu Ser Ser
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Glu Asp	Glu Glu Leu Pro Cys	Phe Gln His Leu Leu	Phe Gly Lys
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Val Asn	Asn Ile Pro Ser Gln	Ser Thr Arg His Ser	Thr Val Ala
1235	1240	1245	
Thr Glu	Cys Leu Ser Lys Asn	Thr Glu Glu Asn Leu	Leu Ser Leu
1250	1255	1260	
Lys Asn	Ser Leu Asn Asp Cys	Ser Asn Gln Val Ile	Leu Ala Lys
1265	1270	1275	
Ala Ser	Gln Glu His His Leu	Ser Glu Glu Thr Lys	Cys Ser Ala
1280	1285	1290	
Ser Leu	Phe Ser Ser Gln Cys	Ser Glu Leu Glu Asp	Leu Thr Ala
1295	1300	1305	
Asn Thr	Asn Thr Gln Asp Pro	Phe Leu Ile Gly Ser	Ser Lys Gln
1310	1315	1320	
Met Arg	His Gln Ser Glu Ser	Gln Gly Val Gly Leu	Ser Asp Lys
1325	1330	1335	
Glu Leu	Val Ser Asp Asp Glu	Glu Arg Gly Thr Gly	Leu Glu Glu
1340	1345	1350	
Asn Asn	Gln Glu Glu Gln Ser	Met Asp Ser Asn Leu	Gly Glu Ala
1355	1360	1365	
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Thr Met Gln His Asn Leu Ile Lys Leu Gln Gln Glu Met Ala Glu				
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Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln Pro Ser Asn Ser				
1415		1420		1425
Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu Asp Leu Arg				
1430		1435		1440
Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr Ser Gln				
1445		1450		1455
Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu Ser				
1460		1465		1470
Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn				
1475		1480		1485
Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser				
1490		1495		1500
Leu Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln				
1505		1510		1515
Asn Arg Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp				
1520		1525		1530
Val Glu Glu Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr				
1535		1540		1545
Glu Thr Ser Tyr Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr				
1550		1555		1560
Leu Glu Ser Gly Ile Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp				
1565		1570		1575
Pro Ser Glu Asp Arg Ala Pro Glu Ser Ala Arg Val Gly Asn Ile				
1580		1585		1590

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1625						1630					1635			
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1670						1675					1680			
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Val	Ser	Tyr	Phe	Trp	Val	Thr	Gln	Ser	Ile	Lys	Glu	Arg	Lys	Met
1715						1720					1725			
Leu	Asn	Glu	His	Asp	Phe	Glu	Val	Arg	Gly	Asp	Val	Val	Asn	Gly
1730						1735					1740			
Arg	Asn	His	Gln	Gly	Pro	Lys	Arg	Ala	Arg	Glu	Ser	Gln	Asp	Arg
1745						1750					1755			
Lys	Ile	Phe	Arg	Gly	Leu	Glu	Ile	Cys	Cys	Tyr	Gly	Pro	Phe	Thr
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1775						1780					1785			
Ala	Ser	Val	Val	Lys	Glu	Leu	Ser	Ser	Phe	Thr	Leu	Gly	Thr	Gly
1790						1795					1800			

Val His Pro Ile Val Val Val Gln Pro Asp Ala Trp Thr Glu Asp
1805 1810 1815

Asn Gly Phe His Ala Ile Gly Gln Met Cys Glu Ala Pro Val Val
1820 1825 1830

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Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His Tyr
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<213> Homo sapiens

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<400> 15
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Ala Asp Ile Gln Gln Met Asn Arg Pro Ser Asn Val Ala His Ile Leu
35           40           45

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Gln Thr Leu Ser Ala Pro Thr Lys Asn Leu Glu Gln Gln Val Asn His
50           55           60

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Ser Gln Gln Gly His Thr Asn Ala Asn Ala Val Leu Phe Ser Gln Val
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Lys Val Thr Pro Glu Thr His Met Leu Gln Gln Gln Gln Gln Ala Gln
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Pro Gln Gln Pro Pro His Pro Phe Ser Gln Gln Gln Gln Gln Gln Gln 130 135 140		
Gln Ala His Pro His Gln Phe Ser Gln Gln Gln Leu Gln Phe Pro Gln 145 150 155 160		
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His Ser Leu Leu Gln Gln Gln Gln Gln Gln Gln Ile Gln Gln Gln Gln 210 215 220		
Leu Gln Arg Met His Gln Gln Gln Gln Gln Gln Gln Met Gln Ser Gln 225 230 235 240		
Thr Ala Pro His Leu Ser Gln Thr Ser Gln Ala Leu Gln His Gln Val 245 250 255		
Pro Pro Gln Gln Pro Pro Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro 260 265 270		
Ser Pro Gln Gln His Gln Leu Phe Gly His Asp Pro Ala Val Glu Ile 275 280 285		
Pro Glu Glu Gly Phe Leu Leu Gly Cys Val Phe Ala Ile Ala Asp Tyr 290 295 300		
Pro Glu Gln Met Ser Asp Lys Gln Leu Leu Ala Thr Trp Lys Arg Ile 305 310 315 320		

Ile Gln Ala His Gly Gly Thr Val Asp Pro Thr Phe Thr Ser Arg Cys
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Thr His Leu Leu Cys Glu Ser Gln Val Ser Ser Ala Tyr Ala Gln Ala
 340 345 350

Ile Arg Glu Arg Lys Arg Cys Val Thr Ala His Trp Leu Asn Thr Val
 355 360 365

Leu Lys Lys Lys Lys Met Val Pro Pro His Arg Ala Leu His Phe Pro
 370 375 380

Val Ala Phe Pro Pro Gly Gly Lys Pro Cys Ser Gln His Ile Ile Ser
 385 390 395 400

Val Thr Gly Phe Val Asp Ser Asp Arg Asp Asp Leu Lys Leu Met Ala
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Tyr Leu Ala Gly Ala Lys Tyr Thr Gly Tyr Leu Cys Arg Ser Asn Thr
 420 425 430

Val Leu Ile Cys Lys Glu Pro Thr Gly Leu Lys Tyr Glu Lys Ala Lys
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Glu Trp Arg Ile Pro Cys Val Asn Ala Gln Trp Leu Gly Asp Ile Leu
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Leu Gly Asn Phe Glu Ala Leu Arg Gln Ile Gln Tyr Ser Arg Tyr Thr
 465 470 475 480

Ala Phe Ser Leu Gln Asp Pro Phe Ala Pro Thr Gln His Leu Val Leu
 485 490 495

Asn Leu Leu Asp Ala Trp Arg Val Pro Leu Lys Val Ser Ala Glu Leu
 500 505 510

Leu Met Ser Ile Arg Leu Pro Pro Lys Leu Lys Gln Asn Glu Val Ala
 515 520 525

Asn Val Gln Pro Ser Ser Lys Arg Ala Arg Ile Glu Asp Val Pro Pro
 530 535 540

Pro Thr Lys Lys Leu Thr Pro Glu Leu Thr Pro Phe Val Leu Phe Thr
 545 550 555 560

Gly Phe Glu Pro Val Gln Val Gln Gln Tyr Ile Lys Lys Leu Tyr Ile
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Leu Gly Gly Glu Val Ala Glu Ser Ala Gln Lys Cys Thr His Leu Ile
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Ala Ser Lys Val Thr Arg Thr Val Lys Phe Leu Thr Ala Ile Ser Val
 595 600 605

Val Lys His Ile Val Thr Pro Glu Trp Leu Glu Glu Cys Phe Arg Cys
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Gln Lys Phe Ile Asp Glu Gln Asn Tyr Ile Leu Arg Asp Ala Glu Ala
 625 630 635 640

Glu Val Leu Phe Ser Phe Ser Leu Glu Glu Ser Leu Lys Arg Ala His
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Val Ser Pro Leu Phe Lys Ala Lys Tyr Phe Tyr Ile Thr Pro Gly Ile
 660 665 670

Cys Pro Ser Leu Ser Thr Met Lys Ala Ile Val Glu Cys Ala Gly Gly
 675 680 685

Lys Val Leu Ser Lys Gln Pro Ser Phe Arg Lys Leu Met Glu His Lys
 690 695 700

Gln Asn Ser Ser Leu Ser Glu Ile Ile Leu Ile Ser Cys Glu Asn Asp
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Leu His Leu Cys Arg Glu Tyr Phe Ala Arg Gly Ile Asp Val His Asn
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Ser Tyr Lys Phe Asn
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<400> 16

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 35 40 45

Ile Ile Ser Glu Asp Gly Asp Asn Pro Glu Val Gly Glu Ala Arg Glu
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Val Phe Asp Leu Pro Val Val Lys Pro Ser Trp Val Ile Leu Ser Val
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Gln Cys Gly Thr Leu Leu Pro Val Asn Gly Phe Ser Pro Glu Ser Cys
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Gln Ile Phe Phe Gly Ile Thr Ala Cys Leu Ser Gln Val Ser Ser Glu
 100 105 110

Asp Arg Ser Ala Leu Trp Ala Leu Val Thr Phe Tyr Gly Gly Asp Cys
 115 120 125

Gln Leu Thr Leu Asn Lys Lys Cys Thr His Leu Ile Val Pro Glu Pro
 130 135 140

Lys Gly Glu Lys Tyr Glu Cys Ala Leu Lys Arg Ala Ser Ile Lys Ile
 145 150 155 160

Val Thr Pro Asp Trp Val Leu Asp Cys Val Ser Glu Lys Thr Lys Lys
 165 170 175

Asp Glu Ala Phe Tyr His Pro Arg Leu Ile Ile Tyr Glu Glu Glu Glu
 180 185 190

Glu Glu Glu Glu Glu Glu Glu Glu Val Glu Asn Glu Glu Gln Asp Ser
 195 200 205

Gln Asn Glu Gly Ser Thr Asp Glu Lys Ser Ser Pro Ala Ser Ser Gln
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Glu Gly Ser Pro Ser Gly Asp Gln Gln Phe Ser Pro Lys Ser Asn Thr
 225 230 235 240

Glu Lys Ser Lys Gly Glu Leu Met Phe Asp Asp Ser Ser Asp Ser Ser
 245 250 255

Pro Glu Lys Gln Glu Arg Asn Leu Asn Trp Thr Pro Ala Glu Val Pro
 260 265 270

Gln Leu Ala Ala Ala Lys Arg Arg Leu Pro Gln Gly Lys Glu Pro Gly
 275 280 285

Leu Ile Asn Leu Cys Ala Asn Val Pro Pro Val Pro Gly Asn Ile Leu
 290 295 300

Pro Pro Glu Val Arg Gly Asn Leu Met Ala Ala Gly Gln Asn Leu Gln
 305 310 315 320

Ser Ser Glu Arg Ser Glu Met Ile Ala Thr Trp Ser Pro Ala Val Arg
 325 330 335

Thr Leu Arg Asn Ile Thr Asn Asn Ala Asp Ile Gln Gln Met Asn Arg
 340 345 350

Pro Ser Asn Val Ala His Ile Leu Gln Thr Leu Ser Ala Pro Thr Lys
 355 360 365

Asn Leu Glu Gln Gln Val Asn His Ser Gln Gln Gly His Thr Asn Ala
 370 375 380

Asn Ala Val Leu Phe Ser Gln Val Lys Val Thr Pro Glu Thr His Met
 385 390 395 400

Leu Gln Gln Gln Gln Gln Ala Gln Gln Gln Gln Gln Gln His Pro Val
 405 410 415

Leu His Leu Gln Pro Gln Gln Ile Met Gln Leu Gln Gln Gln Gln Gln
 420 425 430

Gln Gln Ile Ser Gln Gln Pro Tyr Pro Gln Gln Pro Pro His Pro Phe
 435 440 445

Ser Gln Gln Gln Gln Gln Gln Gln Gln Ala His Pro His Gln Phe Ser
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Gln Gln Gln Leu Gln Phe Pro Gln Gln Gln Leu His Pro Pro Gln Gln
 465 470 475 480

Leu His Arg Pro Gln Gln Gln Leu Gln Pro Phe Gln Gln Gln His Ala
 485 490 495

Leu Gln Gln Gln Phe His Gln Leu Gln Gln His Gln Leu Gln Gln Gln
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Gln Leu Ala Gln Leu Gln Gln Gln His Ser Leu Leu Gln Gln Gln Gln
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Gln Gln Gln Ile Gln Gln Gln Gln Leu Gln Arg Met His Gln Gln Gln
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Gln Gln Gln Gln Met Gln Ser Gln Thr Ala Pro His Leu Ser Gln Thr
 545 550 555 560

Ser Gln Ala Leu Gln His Gln Val Pro Pro Gln Gln Pro Pro Gln Gln
 565 570 575

Gln Gln Gln Gln Gln Pro Pro Pro Ser Pro Gln Gln His Gln Leu Phe
 580 585 590

Gly His Asp Pro Ala Val Glu Ile Pro Glu Glu Gly Phe Leu Leu Gly
 595 600 605

Cys Val Phe Ala Ile Ala Asp Tyr Pro Glu Gln Met Ser Asp Lys Gln
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Leu Leu Ala Thr Trp Lys Arg Ile Ile Gln Ala His Gly Gly Thr Val
 625 630 635 640

Asp Pro Thr Phe Thr Ser Arg Cys Thr His Leu Leu Cys Glu Ser Gln
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Val Ser Ser Ala Tyr Ala Gln Ala Ile Arg Glu Arg Lys Arg Cys Val
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Thr Ala His Trp Leu Asn Thr Val Leu Lys Lys Lys Lys Met Val Pro
 675 680 685

Pro His Arg Ala Leu His Phe Pro Val Ala Phe Pro Pro Gly Gly Lys
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Pro Cys Ser Gln His Ile Ile Ser Val Thr Gly Phe Val Asp Ser Asp
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Gly Tyr Leu Cys Arg Ser Asn Thr Val Leu Ile Cys Lys Glu Pro Thr
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Gly Leu Lys Tyr Glu Lys Ala Lys Glu Trp Arg Ile Pro Cys Val Asn
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Ala Gln Trp Leu Gly Asp Ile Leu Leu Gly Asn Phe Glu Ala Leu Arg
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Gln Ile Gln Tyr Ser Arg Tyr Thr Ala Phe Ser Leu Gln Asp Pro Phe
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Ala Pro Thr Gln His Leu Val Leu Asn Leu Leu Asp Ala Trp Arg Val
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Pro Leu Lys Val Ser Ala Glu Leu Leu Met Ser Ile Arg Leu Pro Pro
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Lys Leu Lys Gln Asn Glu Val Ala Asn Val Gln Pro Ser Ser Lys Arg
 835 840 845

Ala Arg Ile Glu Asp Val Pro Pro Pro Thr Lys Lys Leu Thr Pro Glu
 850 855 860

Leu Thr Pro Phe Val Leu Phe Thr Gly Phe Glu Pro Val Gln Val Gln
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Gln Tyr Ile Lys Lys Leu Tyr Ile Leu Gly Gly Glu Val Ala Glu Ser

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Ala Gln Lys Cys Thr His Leu Ile	Ala Ser Lys Val Thr Arg Thr Val	
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Lys Phe Leu Thr Ala Ile Ser Val Val Lys His Ile Val Thr Pro Glu		
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Trp Leu Glu Glu Cys Phe Arg Cys Gln Lys Phe Ile Asp Glu Gln Asn		
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Tyr Ile Leu Arg Asp Ala Glu Ala Glu Val Leu Phe Ser Phe Ser Leu		
945	950	955
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Glu Glu Ser Leu Lys Arg Ala His Val Ser Pro Leu Phe Lys Ala Lys		
965	970	975
Tyr Phe Tyr Ile Thr Pro Gly Ile Cys Pro Ser Leu Ser Thr Met Lys		
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Ala Ile Val Glu Cys Ala Gly Gly Lys Val Leu Ser Lys Gln Pro Ser		
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Phe Arg Lys Leu Met Glu His Lys Gln Asn Ser Ser Leu Ser Glu		
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Ile Ile Leu Ile Ser Cys Glu Asn Asp Leu His Leu Cys Arg Glu		
1025	1030	1035
Tyr Phe Ala Arg Gly Ile Asp Val His Asn Ala Glu Phe Val Leu		
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attatcgtcg	acccacgac
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 <213> *Xenopus laevis*

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<211> 2629

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<400> 24

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Met	Tyr	Thr	Leu	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Thr	Ser	Cys	Leu
				245					250					255	
Lys	Glu	Thr	Tyr	Leu	Arg	Ile	Lys	Lys	Asn	Glu	Tyr	Ser	Ile	Pro	Lys
				260			265							270	

His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr
 275 280 285

Asp Pro Thr Ala Arg Pro Thr Ile Asn Glu Leu Leu Asn Asp Glu Phe
 290 295 300

Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr
 305 310 315 320

Ile Pro Pro Arg Phe Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Asn
 325 330 335

Arg Lys Pro Leu Thr Val Leu Asn Lys Gly Leu Glu Asn Pro Leu Pro
 340 345 350

Glu Arg Pro Arg Glu Lys Glu Glu Pro Val Val Arg Glu Thr Gly Glu
 355 360 365

Val Val Asp Cys His Leu Ser Asp Met Leu Gln Gln Leu His Ser Val
 370 375 380

Asn Ala Ser Lys Pro Ser Glu Arg Gly Leu Val Arg Gln Glu Glu Ala
 385 390 395 400

Glu Asp Pro Ala Cys Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp
 405 410 415

Tyr Ser Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val
 420 425 430

Gly Val Leu Phe Asn Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly
 435 440 445

Asp Ser Leu Gln Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr
 450 455 460

Val Ser Ser His Pro Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Lys
 465 470 475 480

Tyr Phe Arg Asn Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn
 485 490 495

Ile Thr Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg
500 505 510

Thr Trp Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly
515 520 525

Ser Val Gln Ile Asn Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys
530 535 540

Pro Leu Met Ala Ala Val Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg
545 550 555 560

Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu
565 570 575

Ala Ser Arg Leu Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser
580 585 590

Ser Arg Ser Ala Ser Asn Arg Leu Lys Ala Ser
595 600

<210> 25
<211> 603
<212> PRT
<213> Mus musculus

<400> 25

Met Asn Ala Ala Ala Lys Ala Gly Lys Leu Ala Arg Ala Pro Ala Asp
1 5 10 15

Leu Gly Lys Gly Gly Val Pro Gly Asp Ala Val Pro Gly Ala Pro Val
20 25 30

Ala Ala Pro Leu Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
35 40 45

Ser Arg Arg Gln Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
50 55 60

Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
65 70 75 80

Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Lys Glu

	85		90		95
Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His	100	105	110		
Val Val Gly Phe His Asp Phe Phe Glu Asp Ser Asp Phe Val Phe Val	115	120	125		
Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg	130	135	140		
Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile	145	150	155	160	
Val Leu Gly Cys Gln Tyr Leu His Arg Asn Gln Val Ile His Arg Asp	165	170	175		
Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile	180	185	190		
Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Glu Gly Glu Arg Lys	195	200	205		
Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Ser	210	215	220		
Lys Lys Gly His Ser Phe Glu Val Asp Val Trp Ser Ile Gly Cys Ile	225	230	235	240	
Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser Cys Leu	245	250	255		
Lys Glu Thr Tyr Leu Arg Ile Lys Lys Asn Glu Tyr Ser Ile Pro Lys	260	265	270		
His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr	275	280	285		
Asp Pro Thr Ala Arg Pro Thr Ile His Glu Leu Leu Asn Asp Glu Phe	290	295	300		
Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr	305	310	315	320	

Ile Pro Pro Arg Phe Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Ser
 325 330 335

Arg Lys Pro Leu Lys Val Leu Asn Lys Gly Val Glu Asn Pro Leu Pro
 340 345 350

Asp Arg Pro Arg Glu Lys Glu Glu Pro Val Val Arg Glu Thr Asn Glu
 355 360 365

Ala Ile Glu Cys His Leu Ser Asp Leu Leu Gln Gln Leu Thr Ser Val
 370 375 380

Asn Ala Ser Lys Pro Ser Glu Arg Gly Leu Val Arg Gln Glu Glu Ala
 385 390 395 400

Glu Asp Pro Ala Cys Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp
 405 410 415

Tyr Ser Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val
 420 425 430

Gly Val Leu Phe Asn Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly
 435 440 445

Asp Ser Leu Gln Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr
 450 455 460

Val Ser Ser His Pro Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Asn
 465 470 475 480

Tyr Phe Arg Asn Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn
 485 490 495

Ile Thr Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg
 500 505 510

Thr Trp Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly
 515 520 525

Thr Val Gln Ile Asn Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys
 530 535 540

Pro Leu Met Ala Ala Val Thr Tyr Ile Asn Glu Lys Arg Asp Phe Gln
 545 550 555 560

Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu
 565 570 575

Ala Ser Arg Leu Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser
 580 585 590

Ser Arg Ser Ala Ser Asn Arg Leu Lys Ala Ser
 595 600

<210> 26
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (3)..(6)
 <223> Xaa = any amino acid except Cys

<220>
 <221> MOD_RES
 <222> (7)..(7)
 <223> PHOSPHORYLATION

<220>
 <221> MISC_FEATURE
 <222> (9)..(12)
 <223> Xaa = any amino acid except Cys

<400> 26

Met Ala Xaa Xaa Xaa Xaa Thr Pro Xaa Xaa Xaa Xaa Ala Lys Lys
 1 5 10 15

<210> 27
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>

<221> MISC_FEATURE
<222> (3)..(6)
<223> Xaa = any amino acid except Cys

<220>
<221> MOD_RES
<222> (7)..(7)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (9)..(12)
<223> Xaa = any amino acid except Cys

<400> 27

Met	Ala	Xaa	Xaa	Xaa	Xaa	Ser	Pro	Xaa	Xaa	Xaa	Xaa	Ala	Lys	Lys
1				5					10					15

<210> 28
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(6)
<223> Xaa = any amino acid except Cys

<220>
<221> MOD_RES
<222> (8)..(8)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (9)..(12)
<223> Xaa = any amino acid except Cys

<400> 28

Met	Ala	Xaa	Xaa	Xaa	Xaa	Ser	Thr	Xaa	Xaa	Xaa	Xaa	Ala	Lys	Lys
1				5					10					15

<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
 <221> MISC_FEATURE
 <222> (3)..(6)
 <223> Xaa = any amino acid except Cys

<220>
 <221> MOD_RES
 <222> (8)..(8)
 <223> PHOSPHORYLATION

<220>
 <221> MISC_FEATURE
 <222> (9)..(12)
 <223> Xaa = any amino acid except Cys

<400> 29

Met	Ala	Xaa	Xaa	Xaa	Xaa	Ser	Ser	Xaa	Xaa	Xaa	Xaa	Ala	Lys	Lys
1				5					10					15

<210> 30
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin-X

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(8)
 <223> Xaa is any amino acid except Cys

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Xaa is a biased mixture of Pro, Leu, Ile, Val, Phe, Met, or Trp

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Xaa is any amino acid except Cys

<220>
 <221> MOD_RES
 <222> (11)..(11)
 <223> Phosphorylated

<220>
 <221> MISC_FEATURE
 <222> (13)..(16)
 <223> Xaa is any amino acid except Cys

<400> 30

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Thr Pro Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Lys Lys Lys
 20

<210> 31
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> X is aminohexanoic acid

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin-X

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(8)
 <223> X is any amino acid except for Cys

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)

<223> X is a biased mixture of Phe, Leu, Ile, Val, Phe, Met, or Trp

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> X is any amino acid except for Cys

<220>
 <221> MISC_FEATURE
 <222> (13)..(16)
 <223> X is any amino acid except for Cys

<400> 31

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Thr Pro Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Lys Lys Lys
 20

<210> 32
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin-X

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(10)
 <223> Xaa is any amino acid except Cys

<220>
 <221> MOD_RES
 <222> (11)..(11)
 <223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE
 <222> (12)..(16)
 <223> Xaa is any amino acid except Cys

<400> 32

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Lys Lys Lys
 20

<210> 33
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin-X

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(10)
 <223> Xaa is any amino acid except Cys

<220>
 <221> MISC_FEATURE
 <222> (12)..(16)
 <223> Xaa is any amino acid except Cys

<400> 33

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Lys Lys Lys
 20

<210> 34
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 34

Met	Ala	Gly	Pro	Met	Gln	Ser	Thr	Pro	Leu	Asn	Gly	Ala	Lys	Lys
1				5					10					15

<210> 35
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin-X

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa = aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(9)
 <223> Xaa is any amino acid except Cys

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Xaa is a biased mixture of Ala, Ile, Leu, Met, Asn, Pro, Ser, Thr, or Val

<220>
 <221> MISC_FEATURE
 <222> (11)..(11)
 <223> Xaa is phosphorylated Ser or phosphorylated Thr

<220>
 <221> MISC_FEATURE

<222> (13)..(13)
 <223> Xaa is biased mixture of 25% Glu and 75% any amino acid except
 Arg, Cys, His, or Lys

<220>
 <221> MISC_FEATURE
 <222> (14)..(16)
 <223> Xaa is any amino acid except Cys

<400> 35

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Lys Lys Lys
 20

<210> 36
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Biotin - X

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa is aminohexanoic acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(10)
 <223> Xaa is any amino acid except for Cys

<220>
 <221> MOD_RES
 <222> (11)..(11)
 <223> Phosphorylated Ser

<220>
 <221> MISC_FEATURE
 <222> (12)..(16)
 <223> Xaa is any amino acid except for Cys

<400> 36

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Ala Lys Lys Lys
20

<210> 37

<211> 2089

<212> PRT

<213> Homo sapiens

<400> 37

Met Glu Asp Thr Gln Ala Ile Asp Trp Asp Val Glu Glu Glu Glu Glu
1 5 10 15

Thr Glu Gln Ser Ser Glu Ser Leu Arg Cys Asn Val Glu Pro Val Gly
20 25 30

Arg Leu His Ile Phe Ser Gly Ala His Gly Pro Glu Lys Asp Phe Pro
35 40 45

Leu His Leu Gly Lys Asn Val Val Gly Arg Met Pro Asp Cys Ser Val
50 55 60

Ala Leu Pro Phe Pro Ser Ile Ser Lys Gln His Ala Glu Ile Glu Ile
65 70 75 80

Leu Ala Trp Asp Lys Ala Pro Ile Leu Arg Asp Cys Gly Ser Leu Asn
85 90 95

Gly Thr Gln Ile Leu Arg Pro Pro Lys Val Leu Ser Pro Gly Val Ser
100 105 110

His Arg Leu Arg Asp Gln Glu Leu Ile Leu Phe Ala Asp Leu Leu Cys
115 120 125

Gln Tyr His Arg Leu Asp Val Ser Leu Pro Phe Val Ser Arg Gly Pro
130 135 140

Leu Thr Val Glu Glu Thr Pro Arg Val Gln Gly Glu Thr Gln Pro Gln
145 150 155 160

Arg	Leu	Leu	Leu	Ala	Glu	Asp	Ser	Glu	Glu	Glu	Val	Asp	Phe	Leu	Ser	165	170	175
Glu	Arg	Arg	Met	Val	Lys	Lys	Ser	Arg	Thr	Thr	Ser	Ser	Ser	Val	Ile	180	185	190
Val	Pro	Glu	Ser	Asp	Glu	Glu	Gly	His	Ser	Pro	Val	Leu	Gly	Gly	Leu	195	200	205
Gly	Pro	Pro	Phe	Ala	Phe	Asn	Leu	Asn	Ser	Asp	Thr	Asp	Val	Glu	Glu	210	215	220
Gly	Gln	Gln	Pro	Ala	Thr	Glu	Glu	Ala	Ser	Ser	Ala	Ala	Arg	Arg	Gly	225	230	235
Ala	Thr	Val	Glu	Ala	Lys	Gln	Ser	Glu	Ala	Glu	Val	Val	Thr	Glu	Ile	245	250	255
Gln	Leu	Glu	Lys	Asp	Gln	Pro	Leu	Val	Lys	Glu	Arg	Asp	Asn	Asp	Thr	260	265	270
Lys	Val	Lys	Arg	Gly	Ala	Gly	Asn	Gly	Val	Val	Pro	Ala	Gly	Val	Ile	275	280	285
Leu	Glu	Arg	Ser	Gln	Pro	Pro	Gly	Glu	Asp	Ser	Asp	Thr	Asp	Val	Asp	290	295	300
Asp	Asp	Ser	Arg	Pro	Pro	Gly	Arg	Pro	Ala	Glu	Val	His	Leu	Glu	Arg	305	310	315
Ala	Gln	Pro	Phe	Gly	Phe	Ile	Asp	Ser	Asp	Thr	Asp	Ala	Glu	Glu	Glu	325	330	335
Arg	Ile	Pro	Ala	Thr	Pro	Val	Val	Ile	Pro	Met	Lys	Lys	Arg	Lys	Ile	340	345	350
Phe	His	Gly	Val	Gly	Thr	Arg	Gly	Pro	Gly	Ala	Pro	Gly	Leu	Ala	His	355	360	365
Leu	Gln	Glu	Ser	Gln	Ala	Gly	Ser	Asp	Thr	Asp	Val	Glu	Glu	Gly	Lys	370	375	380

Ala Pro Gln Ala Val Pro Leu Glu Lys Ser Gln Ala Ser Met Val Ile
 385 390 395 400

Asn Ser Asp Thr Asp Asp Glu Glu Glu Val Ser Ala Ala Leu Thr Leu
 405 410 415

Ala His Leu Lys Glu Ser Gln Pro Ala Ile Trp Asn Arg Asp Ala Glu
 420 425 430

Glu Asp Met Pro Gln Arg Val Val Leu Leu Gln Arg Ser Gln Thr Thr
 435 440 445

Thr Glu Arg Asp Ser Asp Thr Asp Val Glu Glu Glu Glu Leu Pro Val
 450 455 460

Glu Asn Arg Glu Ala Val Leu Lys Asp His Thr Lys Ile Arg Ala Leu
 465 470 475 480

Val Arg Ala His Ser Glu Lys Asp Gln Pro Pro Phe Gly Asp Ser Asp
 485 490 495

Asp Ser Val Glu Ala Asp Lys Ser Ser Pro Gly Ile His Leu Glu Arg
 500 505 510

Ser Gln Ala Ser Thr Thr Val Asp Ile Asn Thr Gln Val Glu Lys Glu
 515 520 525

Val Pro Pro Gly Ser Ala Ile Met His Ile Lys Lys His Gln Val Ser
 530 535 540

Val Glu Gly Thr Asn Gln Thr Asp Val Lys Ala Val Gly Gly Pro Ala
 545 550 555 560

Lys Leu Leu Val Val Ser Leu Glu Glu Ala Trp Pro Leu His Gly Asp
 565 570 575

Cys Glu Thr Asp Ala Glu Glu Gly Thr Ser Leu Thr Ala Ser Val Val
 580 585 590

Ala Asp Val Arg Lys Ser Gln Leu Pro Ala Glu Gly Asp Ala Gly Ala
 595 600 605

Glu Trp Ala Ala Ala Val Leu Lys Gln Glu Arg Ala His Glu Val Gly

610	615	620
Ala Gln Gly Gly Pro Pro Val Ala Gln Val Glu Gln Asp Leu Pro Ile		
625	630	635 640
Ser Arg Glu Asn Leu Thr Asp Leu Val Val Asp Thr Asp Thr Leu Gly		
	645	650 655
Glu Ser Thr Gln Pro Gln Arg Glu Gly Ala Gln Val Pro Thr Gly Arg		
	660	665 670
Glu Arg Glu Gln His Val Gly Gly Thr Lys Asp Ser Glu Asp Asn Tyr		
	675	680 685
Gly Asp Ser Glu Asp Leu Asp Leu Gln Ala Thr Gln Cys Phe Leu Glu		
	690	695 700
Asn Gln Gly Leu Glu Ala Val Gln Ser Met Glu Asp Glu Pro Thr Gln		
705	710	715 720
Ala Phe Met Leu Thr Pro Pro Gln Glu Leu Gly Pro Ser His Cys Ser		
	725	730 735
Phe Gln Thr Thr Gly Thr Leu Asp Glu Pro Trp Glu Val Leu Ala Thr		
	740	745 750
Gln Pro Phe Cys Leu Arg Glu Ser Glu Asp Ser Glu Thr Gln Pro Phe		
	755	760 765
Asp Thr His Leu Glu Ala Tyr Gly Pro Cys Leu Ser Pro Pro Arg Ala		
	770	775 780
Ile Pro Gly Asp Gln His Pro Glu Ser Pro Val His Thr Glu Pro Met		
785	790	795 800
Gly Ile Gln Gly Arg Gly Arg Gln Thr Val Asp Lys Val Met Gly Ile		
	805	810 815
Pro Lys Glu Thr Ala Glu Arg Val Gly Pro Glu Arg Gly Pro Leu Glu		
	820	825 830
Arg Glu Thr Glu Lys Leu Leu Pro Glu Arg Gln Thr Asp Val Thr Gly		
	835	840 845

Glu Glu Glu Leu Thr Lys Gly Lys Gln Asp Arg Glu Gln Lys Gln Leu
 850 855 860

Leu Ala Arg Asp Thr Gln Arg Gln Glu Ser Asp Lys Asn Gly Glu Ser
 865 870 875 880

Ala Ser Pro Glu Arg Asp Arg Glu Ser Leu Lys Val Glu Ile Glu Thr
 885 890 895

Ser Glu Glu Ile Gln Glu Lys Gln Val Gln Lys Gln Thr Leu Pro Ser
 900 905 910

Lys Ala Phe Glu Arg Glu Val Glu Arg Pro Val Ala Asn Arg Glu Cys
 915 920 925

Asp Pro Ala Glu Leu Glu Glu Lys Val Pro Lys Val Ile Leu Glu Arg
 930 935 940

Asp Thr Gln Arg Gly Glu Pro Glu Gly Gly Ser Gln Asp Gln Lys Gly
 945 950 955 960

Gln Ala Ser Ser Pro Thr Pro Glu Pro Gly Val Gly Ala Gly Asp Leu
 965 970 975

Pro Gly Pro Thr Ser Ala Pro Val Pro Ser Gly Ser Gln Ser Gly Gly
 980 985 990

Arg Gly Ser Pro Val Ser Pro Arg Arg His Gln Lys Gly Leu Leu Asn
 995 1000 1005

Cys Lys Met Pro Pro Ala Glu Lys Ala Ser Arg Ile Arg Ala Ala
 1010 1015 1020

Glu Lys Val Ser Arg Gly Asp Gln Glu Ser Pro Asp Ala Cys Leu
 1025 1030 1035

Pro Pro Ala Val Pro Glu Ala Pro Ala Pro Pro Gln Lys Pro Leu
 1040 1045 1050

Asn Ser Gln Ser Gln Lys His Leu Ala Pro Pro Pro Leu Leu Ser
 1055 1060 1065

Pro	Leu	Leu	Pro	Ser	Ile	Lys	Pro	Thr	Val	Arg	Lys	Thr	Arg	Gln
1070						1075					1080			
Asp	Gly	Ser	Gln	Glu	Ala	Pro	Glu	Ala	Pro	Leu	Ser	Ser	Glu	Leu
1085						1090					1095			
Glu	Pro	Phe	His	Pro	Lys	Pro	Lys	Ile	Arg	Thr	Arg	Lys	Ser	Ser
1100						1105					1110			
Arg	Met	Thr	Pro	Phe	Pro	Ala	Thr	Ser	Ala	Ala	Pro	Glu	Pro	His
1115						1120					1125			
Pro	Ser	Thr	Ser	Thr	Ala	Gln	Pro	Val	Thr	Pro	Lys	Pro	Thr	Ser
1130						1135					1140			
Gln	Ala	Thr	Arg	Ser	Arg	Thr	Asn	Arg	Ser	Ser	Val	Lys	Thr	Pro
1145						1150					1155			
Glu	Pro	Val	Val	Pro	Thr	Ala	Pro	Glu	Leu	Gln	Pro	Ser	Thr	Ser
1160						1165					1170			
Thr	Asp	Gln	Pro	Val	Thr	Ser	Glu	Pro	Thr	Ser	Gln	Val	Thr	Arg
1175						1180					1185			
Gly	Arg	Lys	Ser	Arg	Ser	Ser	Val	Lys	Thr	Pro	Glu	Thr	Val	Val
1190						1195					1200			
Pro	Thr	Ala	Leu	Glu	Leu	Gln	Pro	Ser	Thr	Ser	Thr	Asp	Arg	Pro
1205						1210					1215			
Val	Thr	Ser	Glu	Pro	Thr	Ser	Gln	Ala	Thr	Arg	Gly	Arg	Lys	Asn
1220						1225					1230			
Arg	Ser	Ser	Val	Lys	Thr	Pro	Glu	Pro	Val	Val	Pro	Thr	Ala	Pro
1235						1240					1245			
Glu	Leu	Gln	Pro	Ser	Thr	Ser	Thr	Asp	Gln	Pro	Val	Thr	Ser	Glu
1250						1255					1260			
Pro	Thr	Tyr	Gln	Ala	Thr	Arg	Gly	Arg	Lys	Asn	Arg	Ser	Ser	Val
1265						1270					1275			

Lys	Thr	Pro	Glu	Pro	Val	Val	Pro	Thr	Ala	Pro	Glu	Leu	Arg	Pro
1280						1285					1290			
Ser	Thr	Ser	Thr	Asp	Arg	Pro	Val	Thr	Pro	Lys	Pro	Thr	Ser	Arg
1295						1300					1305			
Thr	Thr	Arg	Ser	Arg	Thr	Asn	Met	Ser	Ser	Val	Lys	Thr	Pro	Glu
1310						1315					1320			
Thr	Val	Val	Pro	Thr	Ala	Pro	Glu	Leu	Gln	Ile	Ser	Thr	Ser	Thr
1325						1330					1335			
Asp	Gln	Pro	Val	Thr	Pro	Lys	Pro	Thr	Ser	Arg	Thr	Thr	Arg	Ser
1340						1345					1350			
Arg	Thr	Asn	Met	Ser	Ser	Val	Lys	Asn	Pro	Glu	Ser	Thr	Val	Pro
1355						1360					1365			
Ile	Ala	Pro	Glu	Leu	Pro	Pro	Ser	Thr	Ser	Thr	Glu	Gln	Pro	Val
1370						1375					1380			
Thr	Pro	Glu	Pro	Thr	Ser	Arg	Ala	Thr	Arg	Gly	Arg	Lys	Asn	Arg
1385						1390					1395			
Ser	Ser	Gly	Lys	Thr	Pro	Glu	Thr	Leu	Val	Pro	Thr	Ala	Pro	Lys
1400						1405					1410			
Leu	Glu	Pro	Ser	Thr	Ser	Thr	Asp	Gln	Pro	Val	Thr	Pro	Glu	Pro
1415						1420					1425			
Thr	Ser	Gln	Ala	Thr	Arg	Gly	Arg	Thr	Asn	Arg	Ser	Ser	Val	Lys
1430						1435					1440			
Thr	Pro	Glu	Thr	Val	Val	Pro	Thr	Ala	Pro	Glu	Leu	Gln	Pro	Ser
1445						1450					1455			
Thr	Ser	Thr	Asp	Gln	Pro	Val	Thr	Pro	Glu	Pro	Thr	Ser	Gln	Ala
1460						1465					1470			
Thr	Arg	Gly	Arg	Thr	Asp	Arg	Ser	Ser	Val	Lys	Thr	Pro	Glu	Thr
1475						1480					1485			
Val	Val	Pro	Thr	Ala	Pro	Glu	Leu	Gln	Ala	Ser	Ala	Ser	Thr	Asp

1490		1495		1500
Gln Pro Val Thr Ser Glu	Pro Thr Ser Arg Thr	Thr Arg Gly Arg		
1505	1510	1515		
Lys Asn Arg Ser Ser Val	Lys Thr Pro Glu Thr	Val Val Pro Ala		
1520	1525	1530		
Ala Pro Glu Leu Gln Pro	Pro Thr Ser Thr Asp	Arg Pro Val Thr		
1535	1540	1545		
Pro Glu Pro Thr Ser Arg	Ala Thr Arg Gly Arg	Thr Asn Arg Ser		
1550	1555	1560		
Ser Val Lys Thr Pro Glu	Ser Ile Val Pro Ile	Ala Pro Glu Leu		
1565	1570	1575		
Gln Pro Ser Thr Ser Arg	Asn Gln Leu Val Thr	Pro Glu Pro Thr		
1580	1585	1590		
Ser Arg Ala Thr Arg Cys	Arg Thr Asn Arg Ser	Ser Val Lys Thr		
1595	1600	1605		
Pro Glu Pro Val Val Pro	Thr Ala Pro Glu Pro	His Pro Thr Thr		
1610	1615	1620		
Ser Thr Asp Gln Pro Val	Thr Pro Lys Leu Thr	Ser Arg Ala Thr		
1625	1630	1635		
Arg Arg Lys Thr Asn Arg	Ser Ser Val Lys Thr	Pro Lys Pro Val		
1640	1645	1650		
Glu Pro Ala Ala Ser Asp	Leu Glu Pro Phe Thr	Pro Thr Asp Gln		
1655	1660	1665		
Ser Val Thr Pro Glu Ala	Ile Ala Gln Gly Gly	Gln Ser Lys Thr		
1670	1675	1680		
Leu Arg Ser Ser Thr Val	Arg Ala Met Pro Val	Pro Thr Thr Pro		
1685	1690	1695		
Glu Phe Gln Ser Pro Val	Thr Thr Asp Gln Pro	Ile Ser Pro Glu		
1700	1705	1710		

Pro	Ile	Thr	Gln	Pro	Ser	Cys	Ile	Lys	Arg	Gln	Arg	Ala	Ala	Gly
1715						1720					1725			
Asn	Pro	Gly	Ser	Leu	Ala	Ala	Pro	Ile	Asp	His	Lys	Pro	Cys	Ser
1730						1735					1740			
Ala	Pro	Leu	Glu	Pro	Lys	Ser	Gln	Ala	Ser	Arg	Asn	Gln	Arg	Trp
1745						1750					1755			
Gly	Ala	Val	Arg	Ala	Ala	Glu	Ser	Leu	Thr	Ala	Ile	Pro	Glu	Pro
1760						1765					1770			
Ala	Ser	Pro	Gln	Leu	Leu	Glu	Thr	Pro	Ile	His	Ala	Ser	Gln	Ile
1775						1780					1785			
Gln	Lys	Val	Glu	Pro	Ala	Gly	Arg	Ser	Arg	Phe	Thr	Pro	Glu	Leu
1790						1795					1800			
Gln	Pro	Lys	Ala	Ser	Gln	Ser	Arg	Lys	Arg	Ser	Leu	Ala	Thr	Met
1805						1810					1815			
Asp	Ser	Pro	Pro	His	Gln	Lys	Gln	Pro	Gln	Arg	Gly	Glu	Val	Ser
1820						1825					1830			
Gln	Lys	Thr	Val	Ile	Ile	Lys	Glu	Glu	Glu	Glu	Asp	Thr	Ala	Glu
1835						1840					1845			
Lys	Pro	Gly	Lys	Glu	Glu	Asp	Val	Val	Thr	Pro	Lys	Pro	Gly	Lys
1850						1855					1860			
Arg	Lys	Arg	Asp	Gln	Ala	Glu	Glu	Glu	Pro	Asn	Arg	Ile	Pro	Ser
1865						1870					1875			
Arg	Ser	Leu	Arg	Arg	Thr	Lys	Leu	Asn	Gln	Glu	Ser	Thr	Ala	Pro
1880						1885					1890			
Lys	Val	Leu	Phe	Thr	Gly	Val	Val	Asp	Ala	Arg	Gly	Glu	Arg	Ala
1895						1900					1905			
Val	Leu	Ala	Leu	Gly	Gly	Ser	Leu	Ala	Gly	Ser	Ala	Ala	Glu	Ala
1910						1915					1920			

Ser His Leu Val Thr Asp Arg Ile Arg Arg Thr Val Lys Phe Leu
 1925 1930 1935

Cys Ala Leu Gly Arg Gly Ile Pro Ile Leu Ser Leu Asp Trp Leu
 1940 1945 1950

His Gln Ser Arg Lys Ala Gly Phe Phe Leu Pro Pro Asp Glu Tyr
 1955 1960 1965

Val Val Thr Asp Pro Glu Gln Glu Lys Asn Phe Gly Phe Ser Leu
 1970 1975 1980

Gln Asp Ala Leu Ser Arg Ala Arg Glu Arg Arg Leu Leu Glu Gly
 1985 1990 1995

Tyr Glu Ile Tyr Val Thr Pro Gly Val Gln Pro Pro Pro Pro Gln
 2000 2005 2010

Met Gly Glu Ile Ile Ser Cys Cys Gly Gly Thr Tyr Leu Pro Ser
 2015 2020 2025

Met Pro Arg Ser Tyr Lys Pro Gln Arg Val Val Ile Thr Cys Pro
 2030 2035 2040

Gln Asp Phe Pro His Cys Ser Ile Pro Leu Arg Val Gly Leu Pro
 2045 2050 2055

Leu Leu Ser Pro Glu Phe Leu Leu Thr Gly Val Leu Lys Gln Glu
 2060 2065 2070

Ala Lys Pro Glu Ala Phe Val Leu Ser Pro Leu Glu Met Ser Ser
 2075 2080 2085

Thr

<210> 38
 <211> 1972
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Asp Pro Thr Gly Ser Gln Leu Asp Ser Asp Phe Ser Gln Gln Asp

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Thr	Pro	Cys	Leu
	20		
Ile	Ile	Glu	Asp
		25	
Ser	Gln	Pro	Glu
			30
Ser	Gln	Val	Leu
Glu	Asp	Asp	Ser
	35		
Gly	Ser	His	Phe
		40	
Ser	Met	Leu	Ser
			45
Arg	His	Leu	Pro
Asn	Leu	Gln	Thr
	50		
His	Lys	Glu	Asn
		55	
Pro	Val	Leu	Asp
			60
Val	Val	Ser	Asn
Pro	Glu	Gln	Thr
	65		
Ala	Gly	Glu	Glu
	70		
Arg	Gly	Asp	Gly
		75	
Asn	Ser	Gly	Phe
			80
Asn	Glu	His	Leu
	85		
Lys	Glu	Asn	Lys
			90
Val	Ala	Asp	Pro
			95
Val	Asp	Ser	Ser
Asn	Leu	Asp	Thr
	100		
Cys	Gly	Ser	Ile
			105
Ser	Gln	Val	Ile
			110
Glu	Gln	Leu	Pro
Gln	Pro	Asn	Arg
	115		
Thr	Ser	Ser	Val
			120
Leu	Gly	Met	Ser
			125
Val	Glu	Ser	Ala
Pro	Ala	Val	Glu
	130		
Glu	Glu	Glu	Lys
			135
Gly	Glu	Glu	Leu
			140
Glu	Gln	Lys	Glu
Glu	Lys	Glu	Glu
	145		
Asp	Thr	Ser	Gly
			150
Asn	Thr	Thr	His
			155
Ser	Leu	Gly	Ala
			160
Glu	Asp	Thr	Ala
	165		
Ser	Gln	Leu	Gly
			170
Phe	Gly	Val	Leu
			175
Glu	Leu	Ser	
Gln	Ser	Gln	Asp
	180		
Val	Glu	Glu	Asn
			185
Thr	Val	Pro	Tyr
			190
Glu	Val	Asp	Lys
Glu	Gln	Leu	Gln
	195		
Ser	Val	Thr	Thr
			200
Asn	Ser	Gly	Tyr
			205
Thr	Arg	Leu	Ser
Asp	Val	Asp	Ala
	210		
Asn	Thr	Ala	Ile
			215
Lys	His	Glu	Glu
			220
Gln	Ser	Asn	Glu
Asp	Ile	Pro	Ile
	225		
Ala	Glu	Gln	Ser
			230
Ser	Ser	Lys	Asp
			235
Ile	Pro	Val	Thr
			240
Ala			

Gln Pro Ser Lys Asp Val His Val Val Lys Glu Gln Asn Pro Pro Pro
 245 250 255

Ala Arg Ser Glu Asp Met Pro Phe Ser Pro Lys Ala Ser Val Ala Ala
 260 265 270

Met Glu Ala Lys Glu Gln Leu Ser Ala Gln Glu Leu Met Glu Ser Gly
 275 280 285

Leu Gln Ile Gln Lys Ser Pro Glu Pro Glu Val Leu Ser Thr Gln Glu
 290 295 300

Asp Leu Phe Asp Gln Ser Asn Lys Thr Val Ser Ser Asp Gly Cys Ser
 305 310 315 320

Thr Pro Ser Arg Glu Glu Gly Gly Cys Ser Leu Ala Ser Thr Pro Ala
 325 330 335

Thr Thr Leu His Leu Leu Gln Leu Ser Gly Gln Arg Ser Leu Val Gln
 340 345 350

Asp Ser Leu Ser Thr Asn Ser Ser Asp Leu Val Ala Pro Ser Pro Asp
 355 360 365

Ala Phe Arg Ser Thr Pro Phe Ile Val Pro Ser Ser Pro Thr Glu Gln
 370 375 380

Glu Gly Arg Gln Asp Lys Pro Met Asp Thr Ser Val Leu Ser Glu Glu
 385 390 395 400

Gly Gly Glu Pro Phe Gln Lys Lys Leu Gln Ser Gly Glu Pro Val Glu
 405 410 415

Leu Glu Asn Pro Pro Leu Leu Pro Glu Ser Thr Val Ser Pro Gln Ala
 420 425 430

Ser Thr Pro Ile Ser Gln Ser Thr Pro Val Phe Pro Pro Gly Ser Leu
 435 440 445

Pro Ile Pro Ser Gln Pro Gln Phe Ser His Asp Ile Phe Ile Pro Ser
 450 455 460

Pro Ser Leu Glu Glu Gln Ser Asn Asp Gly Lys Lys Asp Gly Asp Met
 465 470 475 480

His Ser Ser Ser Leu Thr Val Glu Cys Ser Lys Thr Ser Glu Ile Glu
 485 490 495

Pro Lys Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly Asp Ser
 500 505 510

Cys Lys Leu Met Leu Ser Thr Ser Glu Tyr Ser Gln Ser Pro Lys Met
 515 520 525

Glu Ser Leu Ser Ser His Arg Ile Asp Glu Asp Gly Glu Asn Thr Gln
 530 535 540

Ile Glu Asp Thr Glu Pro Met Ser Pro Val Leu Asn Ser Lys Phe Val
 545 550 555 560

Pro Ala Glu Asn Asp Ser Ile Leu Met Asn Pro Ala Gln Asp Gly Glu
 565 570 575

Val Gln Leu Ser Gln Asn Asp Asp Lys Thr Lys Gly Asp Asp Thr Asp
 580 585 590

Thr Arg Asp Asp Ile Ser Ile Leu Ala Thr Gly Cys Lys Gly Arg Glu
 595 600 605

Glu Thr Val Ala Glu Asp Val Cys Ile Asp Leu Thr Cys Asp Ser Gly
 610 615 620

Ser Gln Ala Val Pro Ser Pro Ala Thr Arg Ser Glu Ala Leu Ser Ser
 625 630 635 640

Val Leu Asp Gln Glu Glu Ala Met Glu Ile Lys Glu His His Pro Glu
 645 650 655

Glu Gly Ser Ser Gly Ser Glu Val Glu Glu Ile Pro Glu Thr Pro Cys
 660 665 670

Glu Ser Gln Gly Glu Glu Leu Lys Glu Glu Asn Met Glu Ser Val Pro
 675 680 685

Leu His Leu Ser Leu Thr Glu Thr Gln Ser Gln Gly Leu Cys Leu Gln
 690 695 700

Lys Glu Met Pro Lys Lys Glu Cys Ser Glu Ala Met Glu Val Glu Thr
 705 710 715 720

Ser Val Ile Ser Ile Asp Ser Pro Gln Lys Leu Ala Ile Leu Asp Gln
 725 730 735

Glu Leu Glu His Lys Glu Gln Glu Ala Trp Glu Glu Ala Thr Ser Glu
 740 745 750

Asp Ser Ser Val Val Ile Val Asp Val Lys Glu Pro Ser Pro Arg Val
 755 760 765

Asp Val Ser Cys Glu Pro Leu Glu Gly Val Glu Lys Cys Ser Asp Ser
 770 775 780

Gln Ser Trp Glu Asp Ile Ala Pro Glu Ile Glu Pro Cys Ala Glu Asn
 785 790 795 800

Arg Leu Asp Thr Lys Glu Glu Lys Ser Val Glu Tyr Glu Gly Asp Leu
 805 810 815

Lys Ser Gly Thr Ala Glu Thr Glu Pro Val Glu Gln Asp Ser Ser Gln
 820 825 830

Pro Ser Leu Pro Leu Val Arg Ala Asp Asp Pro Leu Arg Leu Asp Gln
 835 840 845

Glu Leu Gln Gln Pro Gln Thr Gln Glu Lys Thr Ser Asn Ser Leu Thr
 850 855 860

Glu Asp Ser Lys Met Ala Asn Ala Lys Gln Leu Ser Ser Asp Ala Glu
 865 870 875 880

Ala Gln Lys Leu Gly Lys Pro Ser Ala His Ala Ser Gln Ser Phe Cys
 885 890 895

Glu Ser Ser Ser Glu Thr Pro Phe His Phe Thr Leu Pro Lys Glu Gly
 900 905 910

Asp Ile Ile Pro Pro Leu Thr Gly Ala Thr Pro Pro Leu Ile Gly His

915	920	925
Leu Lys Leu Glu Pro Lys Arg His Ser Thr Pro Ile Gly Ile Ser Asn		
930	935	940
Tyr Pro Glu Ser Thr Ile Ala Thr Ser Asp Val Met Ser Glu Ser Met		
945	950	955
		960
Val Glu Thr His Asp Pro Ile Leu Gly Ser Gly Lys Gly Asp Ser Gly		
	965	970
		975
Ala Ala Pro Asp Val Asp Asp Lys Leu Cys Leu Arg Met Lys Leu Val		
	980	985
		990
Ser Pro Glu Thr Glu Ala Ser Glu Glu Ser Leu Gln Phe Asn Leu Glu		
995	1000	1005
Lys Pro Ala Thr Gly Glu Arg Lys Asn Gly Ser Thr Ala Val Ala		
1010	1015	1020
Glu Ser Val Ala Ser Pro Gln Lys Thr Met Ser Val Leu Ser Cys		
1025	1030	1035
Ile Cys Glu Ala Arg Gln Glu Asn Glu Ala Arg Ser Glu Asp Pro		
1040	1045	1050
Pro Thr Thr Pro Ile Arg Gly Asn Leu Leu His Phe Pro Ser Ser		
1055	1060	1065
Gln Gly Glu Glu Glu Lys Glu Lys Leu Glu Gly Asp His Thr Ile		
1070	1075	1080
Arg Gln Ser Gln Gln Pro Met Lys Pro Ile Ser Pro Val Lys Asp		
1085	1090	1095
Pro Val Ser Pro Ala Ser Gln Lys Met Val Ile Gln Gly Pro Ser		
1100	1105	1110
Ser Pro Gln Gly Glu Ala Met Val Thr Asp Val Leu Glu Asp Gln		
1115	1120	1125
Lys Glu Gly Arg Ser Thr Asn Lys Glu Asn Pro Ser Lys Ala Leu		
1130	1135	1140

Ile	Glu	Arg	Pro	Ser	Gln	Asn	Asn	Ile	Gly	Ile	Gln	Thr	Met	Glu
1145						1150					1155			
Cys	Ser	Leu	Arg	Val	Pro	Glu	Thr	Val	Ser	Ala	Ala	Thr	Gln	Thr
1160						1165					1170			
Ile	Lys	Asn	Val	Cys	Glu	Gln	Gly	Thr	Ser	Thr	Val	Asp	Gln	Asn
1175						1180					1185			
Phe	Gly	Lys	Gln	Asp	Ala	Thr	Val	Gln	Thr	Glu	Arg	Gly	Ser	Gly
1190						1195					1200			
Glu	Lys	Pro	Val	Ser	Ala	Pro	Gly	Asp	Asp	Thr	Glu	Ser	Leu	His
1205						1210					1215			
Ser	Gln	Gly	Glu	Glu	Glu	Phe	Asp	Met	Pro	Gln	Pro	Pro	His	Gly
1220						1225					1230			
His	Val	Leu	His	Arg	His	Met	Arg	Thr	Ile	Arg	Glu	Val	Arg	Thr
1235						1240					1245			
Leu	Val	Thr	Arg	Val	Ile	Thr	Asp	Val	Tyr	Tyr	Val	Asp	Gly	Thr
1250						1255					1260			
Glu	Val	Glu	Arg	Lys	Val	Thr	Glu	Glu	Thr	Glu	Glu	Pro	Ile	Val
1265						1270					1275			
Glu	Cys	Gln	Glu	Cys	Glu	Thr	Glu	Val	Ser	Pro	Ser	Gln	Thr	Gly
1280						1285					1290			
Gly	Ser	Ser	Gly	Asp	Leu	Gly	Asp	Ile	Ser	Ser	Phe	Ser	Ser	Lys
1295						1300					1305			
Ala	Ser	Ser	Leu	His	Arg	Thr	Ser	Ser	Gly	Thr	Ser	Leu	Ser	Ala
1310						1315					1320			
Met	His	Ser	Ser	Gly	Ser	Ser	Gly	Lys	Gly	Ala	Gly	Pro	Leu	Arg
1325						1330					1335			
Gly	Lys	Thr	Ser	Gly	Thr	Glu	Pro	Ala	Asp	Phe	Ala	Leu	Pro	Ser
1340						1345					1350			

Ser	Arg	Gly	Gly	Pro	Gly	Lys	Leu	Ser	Pro	Arg	Lys	Gly	Val	Ser
1355						1360					1365			
Gln	Thr	Gly	Thr	Pro	Val	Cys	Glu	Glu	Asp	Gly	Asp	Ala	Gly	Leu
1370						1375					1380			
Gly	Ile	Arg	Gln	Gly	Gly	Lys	Ala	Pro	Val	Thr	Pro	Arg	Gly	Arg
1385						1390					1395			
Gly	Arg	Arg	Gly	Arg	Pro	Pro	Ser	Arg	Thr	Thr	Gly	Thr	Arg	Glu
1400						1405					1410			
Thr	Ala	Val	Pro	Gly	Pro	Leu	Gly	Ile	Glu	Asp	Ile	Ser	Pro	Asn
1415						1420					1425			
Leu	Ser	Pro	Asp	Asp	Lys	Ser	Phe	Ser	Arg	Val	Val	Pro	Arg	Val
1430						1435					1440			
Pro	Asp	Ser	Thr	Arg	Arg	Thr	Asp	Val	Gly	Ala	Gly	Ala	Leu	Arg
1445						1450					1455			
Arg	Ser	Asp	Ser	Pro	Glu	Ile	Pro	Phe	Gln	Ala	Ala	Ala	Gly	Pro
1460						1465					1470			
Ser	Asp	Gly	Leu	Asp	Ala	Ser	Ser	Pro	Gly	Asn	Ser	Phe	Val	Gly
1475						1480					1485			
Leu	Arg	Val	Val	Ala	Lys	Trp	Ser	Ser	Asn	Gly	Tyr	Phe	Tyr	Ser
1490						1495					1500			
Gly	Lys	Ile	Thr	Arg	Asp	Val	Gly	Ala	Gly	Lys	Tyr	Lys	Leu	Leu
1505						1510					1515			
Phe	Asp	Asp	Gly	Tyr	Glu	Cys	Asp	Val	Leu	Gly	Lys	Asp	Ile	Leu
1520						1525					1530			
Leu	Cys	Asp	Pro	Ile	Pro	Leu	Asp	Thr	Glu	Val	Thr	Ala	Leu	Ser
1535						1540					1545			
Glu	Asp	Glu	Tyr	Phe	Ser	Ala	Gly	Val	Val	Lys	Gly	His	Arg	Lys
1550						1555					1560			

Glu	Ser	Gly	Glu	Leu	Tyr	Tyr	Ser	Ile	Glu	Lys	Glu	Gly	Gln	Arg
1565						1570					1575			
Lys	Trp	Tyr	Lys	Arg	Met	Ala	Val	Ile	Leu	Ser	Leu	Glu	Gln	Gly
1580						1585					1590			
Asn	Arg	Leu	Arg	Glu	Gln	Tyr	Gly	Leu	Gly	Pro	Tyr	Glu	Ala	Val
1595						1600					1605			
Thr	Pro	Leu	Thr	Lys	Ala	Ala	Asp	Ile	Ser	Leu	Asp	Asn	Leu	Val
1610						1615					1620			
Glu	Gly	Lys	Arg	Lys	Arg	Arg	Ser	Asn	Val	Ser	Ser	Pro	Ala	Thr
1625						1630					1635			
Pro	Thr	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Arg	Lys	Ile
1640						1645					1650			
Thr	Glu	Ser	Pro	Arg	Ala	Ser	Met	Gly	Val	Leu	Ser	Gly	Lys	Arg
1655						1660					1665			
Lys	Leu	Ile	Thr	Ser	Glu	Glu	Glu	Arg	Ser	Pro	Ala	Lys	Arg	Gly
1670						1675					1680			
Arg	Lys	Ser	Ala	Thr	Val	Lys	Pro	Gly	Ala	Val	Gly	Ala	Gly	Glu
1685						1690					1695			
Phe	Val	Ser	Pro	Cys	Glu	Ser	Gly	Asp	Asn	Thr	Gly	Glu	Pro	Ser
1700						1705					1710			
Ala	Leu	Glu	Glu	Gln	Arg	Gly	Pro	Leu	Pro	Leu	Asn	Lys	Thr	Leu
1715						1720					1725			
Phe	Leu	Gly	Tyr	Ala	Phe	Leu	Leu	Thr	Met	Ala	Thr	Thr	Ser	Asp
1730						1735					1740			
Lys	Leu	Ala	Ser	Arg	Ser	Lys	Leu	Pro	Asp	Gly	Pro	Thr	Gly	Ser
1745						1750					1755			
Ser	Glu	Glu	Glu	Glu	Glu	Phe	Leu	Glu	Ile	Pro	Pro	Phe	Asn	Lys
1760						1765					1770			
Gln	Tyr	Thr	Glu	Ser	Gln	Leu	Arg	Ala	Gly	Ala	Gly	Tyr	Ile	Leu

1775	1780	1785
Glu Asp Phe Asn Glu Ala Gln Cys Asn Thr Ala Tyr Gln Cys Leu 1790 1795 1800		
Leu Ile Ala Asp Gln His Cys Arg Thr Arg Lys Tyr Phe Leu Cys 1805 1810 1815		
Leu Ala Ser Gly Ile Pro Cys Val Ser His Val Trp Val His Asp 1820 1825 1830		
Ser Cys His Ala Asn Gln Leu Gln Asn Tyr Arg Asn Tyr Leu Leu 1835 1840 1845		
Pro Ala Gly Tyr Ser Leu Glu Glu Gln Arg Ile Leu Asp Trp Gln 1850 1855 1860		
Pro Arg Glu Asn Pro Phe Gln Asn Leu Lys Val Leu Leu Val Ser 1865 1870 1875		
Asp Gln Gln Gln Asn Phe Leu Glu Leu Trp Ser Glu Ile Leu Met 1880 1885 1890		
Thr Gly Gly Ala Ala Ser Val Lys Gln His His Ser Ser Ala His 1895 1900 1905		
Asn Lys Asp Ile Ala Leu Gly Val Phe Asp Val Val Val Thr Asp 1910 1915 1920		
Pro Ser Cys Pro Ala Ser Val Leu Lys Cys Ala Glu Ala Leu Gln 1925 1930 1935		
Leu Pro Val Val Ser Gln Glu Trp Val Ile Gln Cys Leu Ile Val 1940 1945 1950		
Gly Glu Arg Ile Gly Phe Lys Gln His Pro Lys Tyr Lys His Asp 1955 1960 1965		
Tyr Val Ser His 1970		

<210> 39
<211> 1309

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 39

Met Ser Gly Gln Leu Val Gln Trp Lys Ser Ser Pro Asp Arg Val Thr
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Gln Ser Ala Ile Lys Glu Ala Leu His Ser Pro Leu Ala Asp Gly Asp
20 25 30

Met Asn Glu Met Asn Val Pro Val Asp Pro Leu Glu Asn Lys Val Asn
35 40 45

Ser Thr Asn Ile Ile Glu Gly Ser Pro Lys Ala Asn Pro Asn Pro Val
50 55 60

Lys Phe Met Asn Thr Ser Glu Ile Phe Gln Lys Ser Leu Gly Leu Leu
65 70 75 80

Asp Glu Ser Pro Arg His Asp Asp Glu Leu Asn Ile Glu Val Gly Asp
85 90 95

Asn Asp Arg Pro Asn Ala Asn Ile Leu His Asn Glu Arg Thr Pro Asp
100 105 110

Leu Asp Arg Ile Ala Asn Phe Phe Lys Ser Asn Arg Thr Pro Gly Lys
115 120 125

Glu Asn Leu Leu Thr Lys Tyr Gln Ser Ser Asp Leu Glu Asp Thr Pro
130 135 140

Leu Met Leu Arg Lys Lys Met Thr Phe Gln Thr Pro Thr Asp Pro Leu
145 150 155 160

Glu Gln Lys Thr Phe Lys Lys Leu Lys Ser Asp Thr Gly Phe Cys Tyr
165 170 175

Tyr Gly Glu Gln Asn Asp Gly Glu Glu Asn Ala Ser Leu Glu Val Thr
180 185 190

Glu Ala Asp Ala Thr Phe Val Gln Met Ala Glu Arg Ser Ala Asp Asn
195 200 205

Tyr Asp Cys Ala Leu Glu Gly Ile Val Thr Pro Lys Arg Tyr Lys Asp
 210 215 220

Glu Leu Ser Lys Ser Gly Gly Met Gln Asp Glu Arg Val Gln Lys Thr
 225 230 235 240

Gln Ile Met Ile Ser Ala Glu Ser Pro Asn Ser Ile Ser Ser Tyr Asp
 245 250 255

Lys Asn Lys Ile Thr Gly Asn Gly Arg Thr Thr Arg Asn Val Asn Lys
 260 265 270

Val Phe Asn Asn Asn Glu Asp Asn Ile Gly Ala Ile Glu Glu Lys Asn
 275 280 285

Pro Val Lys Lys Lys Ser Glu Asn Tyr Ser Ser Asp Asp Leu Arg Glu
 290 295 300

Arg Asn Asn Gln Ile Ile Gln Ser Asn Glu Ser Glu Glu Ile Asn Glu
 305 310 315 320

Leu Glu Lys Asn Leu Asn Val Ser Gly Arg Glu Asn Asp Val Asn Asn
 325 330 335

Leu Asp Ile Asp Ile Asn Ser Ala Val Ser Gly Thr Pro Ser Arg Asn
 340 345 350

Asn Ala Glu Glu Glu Met Tyr Ser Ser Glu Ser Val Asn Asn Arg Glu
 355 360 365

Pro Ser Lys Lys Trp Ile Phe Arg Tyr Ser Lys Asp Lys Thr Glu Asn
 370 375 380

Asn Ser Asn Arg Ser Thr Gln Ile Val Asn Asn Pro Arg Thr Gln Glu
 385 390 395 400

Met Pro Leu Asp Ser Ile Ser Ile Asp Thr Gln Pro Leu Ser Lys Ser
 405 410 415

Phe Asn Thr Glu Thr Asn Asn Glu Leu Glu Thr Gln Ile Ile Val Ser
 420 425 430

Ser Leu Ser Gln Gly Ile Ser Ala Gln Lys Gly Pro Val Phe His Ser

435	440	445
Thr Gly Gln Thr Glu Glu Ile Lys Thr Gln Ile Ile Asn Ser Pro Glu		
450	455	460
Gln Asn Ala Leu Asn Ala Thr Phe Glu Thr Pro Val Thr Leu Ser Arg		
465	470	475
Ile Asn Phe Glu Pro Ile Leu Glu Val Pro Glu Thr Ser Ser Pro Ser		
485	490	495
Lys Asn Thr Met Ser Lys Pro Ser Asn Ser Ser Pro Ile Pro Lys Glu		
500	505	510
Lys Asp Thr Phe Asn Ile His Glu Arg Glu Val Glu Thr Asn Asn Val		
515	520	525
Phe Ser Asn Asp Ile Gln Asn Ser Ser Asn Ala Ala Thr Arg Asp Asp		
530	535	540
Ile Ile Ile Ala Gly Ser Ser Asp Phe Asn Glu Gln Lys Glu Ile Thr		
545	550	555
Asp Arg Ile Tyr Leu Gln Leu Ser Gly Lys Gln Ile Ser Asp Ser Gly		
565	570	575
Ser Asp Glu Thr Glu Arg Met Ser Pro Asn Glu Leu Asp Thr Lys Lys		
580	585	590
Glu Ser Thr Ile Met Ser Glu Val Glu Leu Thr Gln Glu Leu Pro Glu		
595	600	605
Val Glu Glu Gln Gln Asp Leu Gln Thr Ser Pro Lys Lys Leu Val Val		
610	615	620
Glu Glu Glu Thr Leu Met Glu Ile Lys Lys Ser Lys Gly Asn Ser Leu		
625	630	635
Gln Leu His Asp Asp Asn Lys Glu Cys Asn Ser Asp Lys Gln Asp Gly		
645	650	655
Thr Glu Ser Leu Asp Val Ala Leu Ile Glu His Glu Ser Lys Gly Gln		
660	665	670

Ser Ser Glu Leu Gln Lys Asn Leu Met Gln Leu Phe Pro Ser Glu Ser
 675 680 685

Gln Glu Ile Ile Gln Asn Arg Arg Thr Ile Lys Arg Arg Gln Lys Asp
 690 695 700

Thr Ile Glu Ile Gly Glu Glu Glu Glu Asn Arg Ser Thr Lys Thr Ser
 705 710 715 720

Pro Thr Lys His Leu Lys Arg Asn Ser Asp Leu Asp Ala Ala Ser Ile
 725 730 735

Lys Arg Glu Pro Ser Cys Ser Ile Thr Ile Gln Thr Gly Glu Thr Gly
 740 745 750

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<400> 46

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5

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<223> Xaa is phosphorylated Thr or phosphorylated Ser

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<222> (3)..(3)

<223> Xaa is Pro or any amino acid

<400> 52

Ser Xaa Xaa

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<210> 53

<211> 7

<212> PRT

<213> Artificial Sequence

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Leu Leu Cys Ser Thr Pro Asn
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Met Ala Xaa Xaa Xaa Xaa Ser Ser Xaa Xaa Xaa Xaa Ala Lys Lys Lys
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<223> Xaa is phosphorylated Ser or phosphorylated Thr

<400> 55

Arg Xaa Arg Ser Xaa Xaa

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<210> 56

<211> 16

<212> PRT

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<220>

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<222> (8)..(8)

<223> PHOSPHORYLATION

<400> 56

Met Ala Gly Pro Met Gln Ser Thr Pro Leu Asn Gly Ala Tyr Lys Lys

1 5 10 15

<210> 57

<211> 16

<212> PRT

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<222> (3)..(5)

<223> Xaa = any amino acid except Cys

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<223> Xaa = Ala, Ile, Leu, Met, Asn, Pro, Ser, Thr, or Val

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<223> Xaa = phosphorylated Ser or phosphorylated Thr

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<223> Xaa = biased mixture of 25% E and 75% any amino acid except Arg, Cys, His, or Lys

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 Met Ala Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Ala Lys Lys Lys
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<223> Xaa is any amino acid except Cys

<400> 59

Gly Ala Xaa Xaa Xaa Xaa Ser Xaa Xaa Phe Xaa Xaa Ala Tyr Lys Lys
1 5 10 15

Lys

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<212> PRT
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Tyr Asp Ile Xaa Gln Val Phe Pro Phe
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<210> 61
<211> 20
<212> PRT
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 <223> BIOTINYLATION

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 <223> Xaa is aminohexanoic acid

 <220>
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 <222> (7)..(9)
 <223> Xaa is any amino acid except Cys

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 <223> Xaa is a biased mixture of Ala, Ile, Let, Met, Asn, Pro, Ser, Thr, or Val

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 <222> (11)..(11)
 <223> Xaa is phosphorylated Ser or phosphorylated Thr

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 <222> (13)..(13)
 <223> Xaa is biased mixture of 25% E and 75% any amino acid except Arg, Cys, His, or Lys

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 <223> Xaa is any amino acid except Cys

 <400> 61

Xaa Gly Xaa Gly Gly Ala Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
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Ala Lys Lys Lys
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<210> 62
 <211> 16
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<223> Xaa is any amino acid except Cys

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<220>
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<223> Xaa is any amino acid except Cys

<400> 62

Gly Ala Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Ala Lys Lys Lys
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<400> 65

Met Ala Gly Pro Met Gln Ser Ser Pro Leu Asn Gly Ala Tyr Lys Lys
1 5 10 15

<210> 66

<211> 16

<212> PRT

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<222> (8)..(8)

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Met Ala Gly Pro Met Gln Ser Tyr Pro Leu Asn Gly Ala Tyr Lys Lys
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<210> 67

<211> 15

<212> PRT

<213> Artificial Sequence

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<222> (8)..(8)

<223> PHOSPHORYLATION

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Met Ala Gly Pro Met Gln Val Thr Pro Leu Asn Gly Ala Lys Lys
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<210> 68

<211> 16

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<213> Artificial Sequence

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<400> 68

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<223> PHOSPHORYLATION

<400> 69

Met	Ala	Gly	Pro	Met	Gln	Gly	Thr	Pro	Leu	Asn	Gly	Ala	Tyr	Lys	Lys
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<210> 70
<211> 16
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<220>
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Met	Ala	Gly	Pro	Met	Gln	Cys	Thr	Pro	Leu	Asn	Gly	Ala	Tyr	Lys	Lys
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<210> 71
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 <222> (8)..(8)
 <223> PHOSPHORYLATION

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 Met Ala Gly Pro Met Gln Thr Thr Pro Leu Asn Gly Ala Tyr Lys Lys
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<210> 72
 <211> 15
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 <223> PHOSPHORYLATION

<400> 72

 Met Ala Gly Pro Met Gln Ser Thr Asn Leu Asn Gly Ala Lys Lys
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<210> 73
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 73

 Ala Gln Leu Leu Cys Ser Thr Pro Asn Gly Leu Asp Arg
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<210> 74
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 <212> PRT
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<220>
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<400> 74

 Pro Arg Leu Leu Cys Ser Thr Pro Ser Phe Lys Lys Thr

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 <210> 75
 <211> 603
 <212> PRT
 <213> Rattus norvegicus

 <400> 75

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 Leu Gly Lys Gly Gly Val Pro Gly Asp Ala Val Pro Gly Ala Pro Val
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 Ala Ala Pro Leu Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
 35 40 45

 Ser Arg Gln Gln Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
 50 55 60

 Ala Lys Cys Phe Glu Ile Ser Asp Ser Asp Thr Lys Glu Val Phe Pro
 65 70 75 80

 Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Lys Glu
 85 90 95

 Lys Met Ser Met Glu Thr Ser Ile His Arg Ser Leu Glu His Gln His
 100 105 110

 Val Val Gly Phe His Gly Phe Phe Glu Asp Ser Asp Phe Val Phe Val
 115 120 125

 Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg
 130 135 140

 Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
 145 150 155 160

 Val Leu Gly Cys Gln Tyr Leu His Arg Asn Gln Val Ile His Arg Asp
 165 170 175

 Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
 180 185 190

Gly	Asp	Phe	Gly	Leu	Ala	Thr	Lys	Val	Glu	Tyr	Glu	Gly	Glu	Arg	Lys	195	200	205	
Lys	Thr	Leu	Cys	Gly	Thr	Pro	Asn	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Ser	210	215	220	
Lys	Lys	Gly	His	Ser	Phe	Glu	Val	Asp	Val	Trp	Ser	Ile	Gly	Cys	Ile	225	230	235	240
Met	Tyr	Thr	Leu	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Thr	Ser	Cys	Leu	245	250	255	
Lys	Glu	Thr	Tyr	Leu	Arg	Ile	Lys	Lys	Asn	Glu	Tyr	Ser	Ile	Pro	Lys	260	265	270	
His	Ile	Asn	Pro	Val	Ala	Ala	Ser	Leu	Ile	Gln	Lys	Met	Leu	Gln	Thr	275	280	285	
Asp	Pro	Ala	Ala	Arg	Pro	Thr	Ile	His	Glu	Leu	Leu	Asn	Asp	Glu	Phe	290	295	300	
Phe	Thr	Ser	Gly	Tyr	Ile	Pro	Ala	Arg	Leu	Pro	Ile	Thr	Cys	Leu	Thr	305	310	315	320
Ile	Pro	Pro	Arg	Phe	Ser	Ile	Ala	Pro	Ser	Ser	Leu	Asp	Pro	Ser	Asn	325	330	335	
Arg	Lys	Pro	Leu	Thr	Val	Leu	Asn	Lys	Gly	Val	Glu	Asn	Pro	Leu	Pro	340	345	350	
Asp	Arg	Pro	Arg	Glu	Lys	Glu	Glu	Pro	Val	Val	Arg	Glu	Thr	Asn	Glu	355	360	365	
Ala	Ile	Glu	Cys	His	Leu	Ser	Asp	Leu	Leu	Gln	Gln	Leu	Thr	Ser	Val	370	375	380	
Asn	Ala	Ser	Lys	Pro	Ser	Glu	Arg	Gly	Leu	Val	Arg	Gln	Glu	Glu	Ala	385	390	395	400
Glu	Asp	Pro	Ala	Cys	Ile	Pro	Ile	Phe	Trp	Val	Ser	Lys	Trp	Val	Asp	405	410	415	

Tyr Ser Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val
420 425 430

Gly Val Leu Phe Asn Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly
435 440 445

Asp Ser Leu Gln Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr
450 455 460

Val Ser Ser His Pro Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Asn
465 470 475 480

Tyr Phe Arg Asn Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn
485 490 495

Ile Thr Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg
500 505 510

Thr Trp Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly
515 520 525

Thr Val Gln Ile Asn Phe Phe Gln Asp His Thr Lys Leu Ile Arg Gly
530 535 540

Pro Leu Met Ala Ala Val Thr Tyr Ile Asn Glu Lys Arg Asp Phe Arg
545 550 555 560

Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu
565 570 575

Ala Ser Arg Leu Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser
580 585 590

Ser Arg Ser Ala Cys Asn Arg Leu Lys Ala Ser
595 600

<210> 76
<211> 648
<212> PRT
<213> Caenorhabditis elegans

<400> 76

Met Asn Arg Leu Pro Asn Ile Ala Lys Pro Pro Gln Lys Ser Asn Gln
1 5 10 15

Arg Lys Glu Lys Ala Pro Pro Glu Val Pro Ala Leu Ile Ala Asp Lys
 20 25 30

Asp Arg Gly Thr Tyr Tyr Glu Lys Gly Arg Phe Leu Gly Lys Gly Gly
 35 40 45

Phe Ala His Cys Tyr Glu Leu Thr Asn Arg Ala Thr Arg Glu Val Val
 50 55 60

Ala Gly Lys Val Val Pro Lys Ser Met Leu Val Lys Gln Tyr Gln Arg
 65 70 75 80

Asp Lys Met Thr Gln Glu Val Gln Ile His Arg Glu Leu Gly His Ile
 85 90 95

Asn Ile Val Lys Leu Phe Asn Phe Phe Glu Asp Asn Leu Asn Val Tyr
 100 105 110

Ile Thr Leu Glu Leu Cys Ala Arg Arg Ser Leu Met Glu Leu His Lys
 115 120 125

Arg Arg Lys Ala Val Thr Glu Pro Glu Ala Arg Tyr Phe Thr His Gln
 130 135 140

Ile Val Asp Gly Val Leu Tyr Leu His Asp Leu Asn Ile Ile His Arg
 145 150 155 160

Asp Met Lys Leu Gly Asn Leu Phe Leu Asn Asp Asp Leu Val Val Lys
 165 170 175

Ile Gly Asp Phe Gly Leu Ala Thr Thr Val Asn Gly Asp Glu Arg Lys
 180 185 190

Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Asn
 195 200 205

Lys Ala Gly His Ser Phe Glu Val Asp Ile Trp Ala Val Gly Cys Ile
 210 215 220

Leu Tyr Ile Leu Leu Phe Gly Gln Pro Pro Phe Glu Ser Lys Ser Leu
 225 230 235 240

Glu Glu Thr Tyr Ser Arg Ile Arg His Asn Asn Tyr Thr Ile Pro Ser
 245 250 255

Ile Ala Thr Gln Pro Ala Ala Ser Leu Ile Arg Lys Met Leu Asp Pro
 260 265 270

Glu Pro Thr Arg Arg Pro Thr Ala Lys Gln Val Gln Arg Asp Gly Phe
 275 280 285

Phe Lys Ser Gly Phe Met Pro Thr Arg Leu Pro Val Ser Cys Leu Thr
 290 295 300

Met Val Pro Lys Phe Gly Gly His Glu Thr Ser Met Met Glu Glu Asn
 305 310 315 320

Val Ala Pro Arg Gly Val Asp Ala Arg Ser Gln Arg Pro Leu Asn Gly
 325 330 335

Arg Ala Gly Leu Ser Ala Leu Pro Gln His Ile Val Ser Asn Asn Ala
 340 345 350

Asp Arg Glu Arg Ala Gln Gln Gln Ala Ala Glu Ala Thr Phe Arg Glu
 355 360 365

Pro Glu Asp Ala Tyr Leu Ser Gln Leu Phe His Gln Val Ala Val Leu
 370 375 380

Leu Glu Gln Arg Ile Pro Gly Leu Glu Glu Glu Glu Ala Ala Leu Asp
 385 390 395 400

Gly Tyr Gln Ser Pro Glu Cys Leu Pro Val Phe Trp Ile Ser Lys Trp
 405 410 415

Val Asp Tyr Ser Asp Lys Tyr Gly Ile Gly Tyr Gln Leu Cys Asp Asn
 420 425 430

Ser Val Gly Val Leu Phe Asn Asp Asn Ser Arg Ile Met Leu Asp Gln
 435 440 445

Ala Gly Asn Glu Leu Thr Tyr Ile Glu Lys Ser Asn Lys Glu His Tyr
 450 455 460

Phe Ser Met His Ser Gly Glu Met Pro Gly Leu Leu Asn Lys Lys Val
 465 470 475 480

Thr Leu Leu Lys Tyr Phe Arg Ser Tyr Met Asn Asp His Leu Val Lys
 485 490 495

Ala Gly Glu Gly Ser Glu Gln Arg Ala Gly Asp Asp Leu Ala Arg Leu
 500 505 510

Pro Thr Leu Arg Val Trp Phe Arg Thr Lys Ser Ala Ile Val Leu His
 515 520 525

Leu Ser Asn Gly Thr Val Gln Ile Asn Phe Phe Asn Asp His Val Lys
 530 535 540

Met Met Met Cys Pro Leu Met Gln Ala Val Thr Phe Ile Asp Gln Asn
 545 550 555 560

Lys Arg Met Leu Thr Tyr Lys Leu Asn Asn Leu Gln Arg Asn Gly Cys
 565 570 575

Pro Glu Lys Phe Leu His Arg Leu Lys Tyr Ala Lys Thr Met Ile Glu
 580 585 590

Arg Leu Met Ser Asp Ala Asn Val Val Ser Gln Asn Pro Ala Arg Gln
 595 600 605

Pro Asp Met Pro Arg Ser Met Ala Ala Ala Arg Ser Ala Ser Ala Gly
 610 615 620

Ser Arg Gly Pro Asn Gln Ala Ala Ser His Leu Pro Gln Ser Ala Ser
 625 630 635 640

Gly Ser Asn Ile His Pro Arg Arg
 645

<210> 77
 <211> 278
 <212> PRT
 <213> Homo sapiens

<400> 77

Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Asn Arg Lys Pro Leu Thr
 1 5 10 15

Val Leu Asn Lys Gly Leu Glu Asn Pro Leu Pro Glu Arg Pro Arg Glu
 20 25 30

Lys Glu Glu Pro Val Val Arg Glu Thr Gly Glu Val Val Asp Cys His
 35 40 45

Leu Ser Asp Met Leu Gln Gln Leu His Ser Val Asn Ala Ser Lys Pro
 50 55 60

Ser Glu Arg Gly Leu Val Arg Gln Glu Glu Ala Glu Asp Pro Ala Cys
 65 70 75 80

Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr
 85 90 95

Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn
 100 105 110

Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr
 115 120 125

Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro
 130 135 140

Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn Tyr
 145 150 155 160

Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu
 165 170 175

Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr
 180 185 190

Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly Ser Val Gln Ile Asn
 195 200 205

Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys Pro Leu Met Ala Ala
 210 215 220

Val Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser
 225 230 235 240

Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg
245 250 255

Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser
260 265 270

Asn Arg Leu Lys Ala Ser
275

<210> 78
<211> 282
<212> PRT
<213> *Xenopus laevis*

<400> 78

Ser Ile Ala Pro Ser Thr Ile Asp Gln Ser Leu Arg Lys Pro Leu Thr
1 5 10 15

Ala Ile Asn Lys Gly Gln Asp Ser Pro Leu Val Glu Lys Gln Val Ala
20 25 30

Pro Ala Lys Glu Glu Glu Met Gln Gln Pro Glu Phe Thr Glu Pro Ala
35 40 45

Asp Cys Tyr Leu Ser Glu Met Leu Gln Gln Leu Thr Cys Leu Asn Ala
50 55 60

Val Lys Pro Ser Glu Arg Ala Leu Ile Arg Gln Glu Glu Ala Glu Asp
65 70 75 80

Pro Ala Ser Ile Pro Ile Phe Trp Ile Ser Lys Trp Val Asp Tyr Ser
85 90 95

Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val
100 105 110

Leu Phe Asn Asp Ser Thr Arg Leu Ile Met Tyr Asn Asp Gly Asp Ser
115 120 125

Leu Gln Tyr Ile Glu Arg Asn Asn Thr Glu Ser Tyr Leu Asn Val Arg
130 135 140

Ser Tyr Pro Thr Thr Leu Thr Lys Lys Ile Thr Leu Leu Lys Tyr Phe

145		150		155		160
Arg Asn Tyr Met	Ser Glu His Leu Leu Lys Ala Gly Ala Asn Thr Thr					
	165		170		175	
Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Phe Leu Arg Thr Trp						
	180		185		190	
Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly Thr Val						
	195		200		205	
Gln Ile Asn Phe Phe Gln Asp His Thr Lys Ile Ile Leu Cys Pro Leu						
	210		215		220	
Met Ala Ala Val Ser Tyr Ile Asp Glu Lys Arg Glu Phe Arg Thr Tyr						
	225		230		235	240
Lys Leu Ser Leu Ile Gln Glu Phe Gly Cys Cys Lys Glu Leu Ala Ser						
	245		250		255	
Arg Leu Arg Tyr Ala Arg Thr Met Val Glu Lys Leu Gln Ser Ser Lys						
	260		265		270	
Ser Ala Val Ala His Val Lys Ala Ser Ala						
	275		280			
<210> 79						
<211> 279						
<212> PRT						
<213> Drosophila melanogaster						
<400> 79						
Gly Ser Asn Asp Thr Ile Glu Asp Ser Met His Arg Lys Pro Leu Met						
1	5		10		15	
Glu Met Asn Gly Ile Arg Pro Asp Asp Thr Arg Leu Glu Ser Thr Phe						
	20		25		30	
Leu Lys Ala Asn Leu His Asp Ala Ile Thr Ala Ser Ala Gln Val Cys						
	35		40		45	
Arg His Ser Glu Asp Tyr Arg Ser Asp Ile Glu Ser Leu Tyr Gln Gln						
	50		55		60	

Leu Thr Asn Leu Ile Asn Gly Lys Pro Arg Ile Leu Gln Gly Asn Leu
 65 70 75 80

Gly Asp Glu Asn Thr Asp Pro Ala Ala Gln Pro Leu Phe Trp Ile Ser
 85 90 95

Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly Phe Gly Tyr Gln Leu Cys
 100 105 110

Asp Glu Gly Ile Gly Val Met Phe Asn Asp Thr Thr Lys Leu Ile Leu
 115 120 125

Leu Pro Asn Gln Ile Asn Val His Phe Ile Asp Lys Asp Gly Lys Glu
 130 135 140

Thr Tyr Met Thr Thr Thr Asp Tyr Cys Lys Ser Leu Asp Lys Lys Met
 145 150 155 160

Lys Leu Leu Ser Tyr Phe Lys Arg Tyr Met Ile Glu His Leu Val Lys
 165 170 175

Ala Gly Ala Asn Asn Val Asn Ile Glu Ser Asp Gln Ile Ser Arg Met
 180 185 190

Pro His Leu His Ser Trp Phe Arg Thr Thr Cys Ala Val Val Met His
 195 200 205

Leu Thr Asn Gly Ser Val Gln Leu Asn Phe Ser Asp His Met Lys Leu
 210 215 220

Ile Leu Cys Pro Arg Met Ser Ala Ile Thr Tyr Met Asp Gln Glu Lys
 225 230 235 240

Asn Phe Arg Thr Tyr Arg Phe Ser Thr Ile Val Glu Asn Gly Val Ser
 245 250 255

Lys Asp Leu Tyr Gln Lys Ile Arg Tyr Ala Gln Glu Lys Leu Arg Lys
 260 265 270

Met Leu Glu Lys Met Phe Thr
 275

<210> 80
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 80

Ala Gln Leu Leu Cys Ser Thr Pro Asn Gly Leu Asp Arg
 1 5 10

<210> 81
 <211> 13
 <212> PRT
 <213> Xenopus laevis

<400> 81

Pro Arg Leu Leu Cys Ser Thr Pro Ser Phe Lys Lys Thr
 1 5 10

<210> 82
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 82

Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
 1 5 10 15

Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
 20 25 30

Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile
 35 40 45

Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro Asn
 50 55 60

Ser Leu Met Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn Tyr Met
 65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu Gly
 85 90 95

Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr Arg
 100 105 110

Ser Ala Ile Ile Leu His Leu Ser Asn Gly Ser Val Gln Ile Asn Phe
115 120 125

Phe Gln Asp His Ile Lys Leu Ile Leu Cys Pro Leu Met Ala Ala Val
130 135 140

Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser Leu
145 150 155 160

Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr
165 170 175

Ala Arg Thr Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser Asn
180 185 190

Arg Leu Lys Ala Ser
195

<210> 83
<211> 197
<212> PRT
<213> Mus musculus

<400> 83

Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
20 25 30

Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile
35 40 45

Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro Asn
50 55 60

Ser Leu Met Lys Lys Ile Thr Leu Leu Asn Tyr Phe Arg Asn Tyr Met
65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu Gly
85 90 95

Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr Arg
100 105 110

Ser Ala Ile Ile Leu His Leu Ser Asn Gly Thr Val Gln Ile Asn Phe
115 120 125

Phe Gln Asp His Thr Lys Leu Ile Leu Cys Pro Leu Met Ala Ala Val
130 135 140

Thr Tyr Ile Asn Glu Lys Arg Asp Phe Gln Thr Tyr Arg Leu Ser Leu
145 150 155 160

Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr
165 170 175

Ala Arg Thr Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser Asn
180 185 190

Arg Leu Lys Ala Ser
195

<210> 84
<211> 197
<212> PRT
<213> Rattus norvegicus

<400> 84

Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Leu Gly Tyr Asp Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
20 25 30

Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile
35 40 45

Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro Asn
50 55 60

Ser Leu Met Lys Lys Ile Thr Leu Leu Asn Tyr Phe Arg Asn Tyr Met
65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu Gly
85 90 95

Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr Arg
100 105 110

Ser Ala Ile Ile Leu His Leu Ser Asn Gly Thr Val Gln Ile Asn Phe
115 120 125

Phe Gln Asp His Thr Lys Leu Ile Arg Gly Pro Leu Met Ala Ala Val
130 135 140

Thr Tyr Ile Asn Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser Leu
145 150 155 160

Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr
165 170 175

Ala Arg Thr Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Cys Asn
180 185 190

Arg Leu Lys Ala Ser
195

<210> 85
<211> 210
<212> PRT
<213> Caenorhabditis elegans

<400> 85

Pro Val Phe Trp Ile Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Ile Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
20 25 30

Asn Ser Arg Ile Met Leu Asp Gln Ala Gly Asn Glu Leu Thr Tyr Ile
35 40 45

Glu Lys Ser Asn Lys Glu His Tyr Phe Ser Met His Ser Gly Glu Met
50 55 60

Pro Gly Leu Leu Met Lys Lys Asn Thr Leu Leu Lys Tyr Phe Arg Ser
65 70 75 80

Tyr Met Asn Asp His Leu Val Lys Ala Gly Glu Gly Ser Glu Gln Arg
85 90 95

Ala Gly Asp Asp Leu Ala Arg Leu Pro Thr Leu Arg Val Trp Phe Arg
100 105 110

Thr Lys Ser Ala Ile Val Leu His Leu Ser Asn Gly Thr Val Gln Ile
115 120 125

Asn Phe Phe Asn Asp His Val Lys Met Met Met Cys Pro Leu Met Gln
130 135 140

Ala Val Thr Phe Ile Asp Gln Asn Lys Arg Met Leu Thr Tyr Lys Leu
145 150 155 160

Asn Asn Leu Gln Arg Asn Gly Cys Pro Glu Lys Phe Leu His Arg Leu
165 170 175

Lys Tyr Ala Lys Thr Met Ile Glu Arg Leu Met Asp Ser Ala Asn Val
180 185 190

Val Ser Gln Asn Pro Ala Arg Gln Pro Asp Met Pro Arg Ser Met Ala
195 200 205

Ala Ala
210

<210> 86
<211> 189
<212> PRT
<213> Drosophila melanogaster

<400> 86

Pro Leu Phe Trp Ile Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Cys Asp Glu Gly Ile Gly Val Met Phe Asn Asp
20 25 30

Thr Thr Lys Leu Ile Leu Leu Pro Asn Gln Ile Asn Val His Phe Ile
35 40 45

Asp Lys Asp Gly Lys Glu Thr Tyr Met Thr Thr Thr Asp Tyr Cys Lys
50 55 60

Ser Leu Asp Lys Lys Met Lys Leu Leu Ser Tyr Phe Lys Arg Tyr Met
65 70 75 80

Ile Glu His Leu Val Lys Ala Gly Ala Asn Asn Val Asn Ile Glu Ser
85 90 95

Asp Gln Ile Ser Arg Met Pro His Leu His Ser Trp Phe Arg Thr Thr
100 105 110

Cys Ala Val Val Met His Leu Thr Asn Gly Ser Val Gln Leu Asn Phe
115 120 125

Ser Asp His Met Lys Leu Ile Leu Cys Pro Arg Met Ser Ala Ile Thr
130 135 140

Tyr Met Asp Gln Glu Lys Asn Phe Arg Thr Tyr Arg Phe Ser Thr Ile
145 150 155 160

Val Glu Asn Gly Val Ser Lys Asp Leu Tyr Gln Lys Ile Arg Tyr Ala
165 170 175

Gln Glu Lys Leu Arg Lys Met Leu Glu Lys Met Phe Thr
180 185

<210> 87
<211> 198
<212> PRT
<213> Xenopus laevis

<400> 87

Pro Ile Phe Trp Ile Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
20 25 30

Ser Thr Arg Leu Ile Met Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile
35 40 45

Glu Arg Asn Asn Thr Glu Ser Tyr Leu Asn Val Arg Ser Tyr Pro Thr
50 55 60

Thr Leu Thr Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn Tyr Met
65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Asn Thr Thr Pro Arg Glu Gly
85 90 95

Asp Glu Leu Ala Arg Leu Pro Phe Leu Arg Thr Trp Phe Arg Thr Arg
100 105 110

Ser Ala Ile Ile Leu His Leu Ser Asn Gly Thr Val Gln Ile Asn Phe
115 120 125

Phe Gln Asp His Thr Lys Ile Ile Leu Cys Pro Leu Met Ala Ala Val
130 135 140

Ser Tyr Ile Asp Glu Lys Arg Glu Phe Arg Thr Tyr Lys Leu Ser Leu
145 150 155 160

Ile Gln Glu Phe Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr
165 170 175

Ala Arg Thr Met Val Glu Lys Leu Gln Ser Ser Lys Ser Ala Val Ala
180 185 190

His Val Lys Ala Ser Ala
195

<210> 88
<211> 195
<212> PRT
<213> Helicobacter pylori

<400> 88

Pro Ile Leu Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
1 5 10 15

Leu Gly Tyr Gln Leu Cys Asp Gly Ser Val Gly Val Leu Phe Asn Asp
20 25 30

Ser Thr Arg Leu Leu Leu His Ala Asn Ala Asp Thr Leu Glu Tyr Ile
35 40 45

Glu Arg Asp Gly Asn Glu Lys Tyr Cys Arg Leu Gly Ser Tyr Asp Ser
50 55 60

Thr Leu His Lys Lys Val Thr Leu Leu Lys Tyr Phe Arg Asn Tyr Met
65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Ala Met Thr Pro Arg Glu Ser
85 90 95

Asp Ser Met Ala Arg Leu Pro Phe Leu Gln Ser Trp Phe Arg Thr Lys
100 105 110

Ser Ala Ile Val Leu His Leu Ser Asn Gly Thr Val Gln Ile Asn Phe
115 120 125

Phe Glu Asp His Thr Lys Leu Ile Val Cys Pro Met Met Gly Ala Ala
130 135 140

Thr Tyr Ile Asp Ala Lys Arg Asn Phe Arg Thr Phe Arg Leu Asn Leu
145 150 155 160

Ile Glu Lys His Gly Cys Thr Pro Asp Leu Tyr Asp Arg Ile Lys Tyr
165 170 175

Ala Asn Asn Met Val Lys Asn Met Leu Asp Lys Lys Thr Thr Thr Ala
180 185 190

Ala Ala His
195

<210> 89
<211> 186
<212> PRT
<213> Homo sapiens

<400> 89

Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu Phe Asn Asn
20 25 30

Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val His Tyr Tyr
35 40 45

Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp Ala Arg Glu
50 55 60

Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser His Tyr Met
65 70 75 80

Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val Thr Asp Ile
85 90 95

Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser Asp Lys Ala
100 105 110

Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn Phe Tyr His
115 120 125

Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu Tyr Leu Leu
130 135 140

Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg Leu Thr Thr
145 150 155 160

Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg Met Glu Tyr
165 170 175

Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
180 185

<210> 90
<211> 186
<212> PRT
<213> Mus musculus

<400> 90

Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu Phe Asn Asn
20 25 30

Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val His Tyr Tyr
35 40 45

Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp Ala Pro Glu
50 55 60

Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser His Tyr Met
65 70 75 80

Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val Thr Asp Ile
85 90 95

Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser Asp Lys Ala
100 105 110

Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn Phe Tyr His
115 120 125

Asp His Thr Lys Ile Ile Ile Cys Asn Gln Ser Glu Glu Tyr Leu Leu
130 135 140

Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg Leu Thr Thr
145 150 155 160

Leu Leu Met Ser Gly Cys Ser Leu Glu Leu Lys Asn Arg Met Glu Tyr
165 170 175

Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
180 185

<210> 91
<211> 186
<212> PRT
<213> Rattus norvegicus

<400> 91

Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu Phe Asn Asn
20 25 30

Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val His Tyr Tyr
35 40 45

Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp Ala Pro Glu
50 55 60

Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser His Tyr Met
65 70 75 80

Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val Thr Asp Ile
85 90 95

Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser Asp Lys Ala
100 105 110

Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn Phe Tyr His
115 120 125

Asp His Thr Lys Ile Ile Ile Cys Asn Gln Asn Glu Glu Tyr Leu Leu
130 135 140

Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg Leu Thr Thr
145 150 155 160

Leu Leu Met Ser Gly Cys Ser Leu Glu Leu Lys His Arg Met Glu Tyr
165 170 175

Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
180 185

<210> 92
<211> 214
<212> PRT
<213> Caenorhabditis elegans

<400> 92

Pro Ile Phe Trp Val Ser Gln Trp Val His Phe Pro Asn His Gly Ile
1 5 10 15

Gly Tyr Arg Leu Cys Glu Asn Ser Ser Gly Met Leu Phe Asn Asp Asn
20 25 30

Thr Gln Met Lys Val Asn Ser Ala Gly Asn Gln Leu Thr Phe Val Asp
35 40 45

Glu Asn Asn Thr Glu Gln Phe Tyr Thr Met Asn Asp Gln Val Pro Met
50 55 60

Asn Leu Gln Thr Lys Ile Asn Ile Phe Ser Asn Val Gln Ser Tyr Met
65 70 75 80

Asn Thr His Leu Glu Ala Asp Thr His Leu Glu Ala Glu Asp Gln Cys
85 90 95

Val Asn Lys Val Pro Pro Leu Arg Asn Phe Ala Arg Leu Pro Thr Ile
100 105 110

Gln Asn Trp Phe Glu Thr Lys Ser Ala Val Ile Phe His Leu Ser Asn
115 120 125

Gly Thr Val Gln Ile Asn Phe Leu Asp His Val Lys Met Val Leu Cys
130 135 140

Pro Leu Leu Lys Ser Val Thr Phe Ile Glu Glu Asn Lys Arg Val Ser
145 150 155 160

Thr Phe Thr Phe Ala Asn Ile Leu Thr Asn Ser Cys Pro Lys Lys Tyr
165 170 175

Leu Ser Arg Ile Glu Tyr Ala Gln Ala Lys Ile Lys Leu Leu Arg Pro
180 185 190

Thr Asn Asn Gln Glu His Val Val Tyr Val Asp Ser Pro Cys Arg Pro
195 200 205

Thr Thr Ser Asn Thr Ala
210

<210> 93
<211> 187
<212> PRT
<213> Xenopus laevis

<400> 93

Ser Phe His Trp Val Thr Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu Phe Asn Asn
20 25 30

Gly Ala His Met Ser Phe Leu Pro Asp Lys Lys Thr Val His Tyr Tyr
35 40 45

Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Glu Ala Pro Glu
50 55 60

Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser His Tyr Met
65 70 75 80

Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val Thr Asp Val
85 90 95

Cys Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser Asp Lys Ala
100 105 110

Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn Phe Tyr His
115 120 125

Asp His Thr Lys Ile Ile Ile Ala Asn Gln Asn Asp Glu Tyr Val Leu
130 135 140

Thr Tyr Ile Asn Glu Asp Arg Met Ser Thr Thr Phe His Leu Ser Thr
145 150 155 160

Leu Leu Ile Ser Gly Cys Ser Pro Asp Leu Arg Gln Arg Leu Arg Tyr
165 170 175

Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
180 185

<210> 94
<211> 187
<212> PRT
<213> Homo sapiens

<400> 94

Pro Leu Val Trp Phe Ser Glu Trp Val Gly Phe Ser Asn Lys Phe Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val Leu Phe Asn Asp
20 25 30

Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr Val His Tyr Asn
35 40 45

Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly Ala Val Arg Arg
50 55 60

Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe Ala Ser Tyr Met
65 70 75 80

Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser Val Glu Glu Val
85 90 95

Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val Lys Thr Asp Gln
100 105 110

Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln Val Asn Phe Tyr
115 120 125

Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu Pro Leu Leu Val
130 135 140

Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr Leu Ala Ser His
145 150 155 160

Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln Arg Leu Arg Tyr
165 170 175

Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
180 185

<210> 95
<211> 187
<212> PRT
<213> Mus musculus

<400> 95

Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser Asn Lys Phe Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val Leu Phe Asn Asp
20 25 30

Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr Val His Tyr Asn
35 40 45

Pro Thr Ser Thr Lys His Phe Ser Phe Ser Met Gly Ser Val Pro Arg
50 55 60

Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe Ala Ser Tyr Met
65 70 75 80

Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser Val Glu Glu Ala
85 90 95

Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val Lys Thr Asp Gln
100 105 110

Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln Val Asn Phe Tyr
115 120 125

Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu Pro Leu Leu Val
130 135 140

Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr Leu Ala Ser His
145 150 155 160

Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln Arg Leu Arg Tyr
165 170 175

Ala Leu Arg Leu Leu Arg Asp Gln Ser Pro Ala
180 185

<210> 96
<211> 186
<212> PRT
<213> Rattus norvegicus

<400> 96

Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser Asn Lys Phe Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val Leu Phe Asn Asp
20 25 30

Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr Val His Tyr Asn
35 40 45

Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly Ser Val Pro Arg
50 55 60

Ala Leu Arg Pro Gln Leu Gly Ile Leu Arg Tyr Phe Ala Ser Tyr Met
65 70 75 80

Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser Val Glu Glu Val
85 90 95

Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val Lys Thr Asp Gln
100 105 110

Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln Val Asn Phe Tyr
115 120 125

Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu Pro Leu Leu Val
130 135 140

Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr Leu Ala Ser His
145 150 155 160

Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln Arg Leu Arg Tyr
165 170 175

Ala Leu Arg Leu Leu Arg Asp Gln Ser Pro
180 185

<210> 97
<211> 186
<212> PRT
<213> Xenopus laevis

<400> 97

His Phe Val Trp Val Ser Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Phe Gly Tyr Gln Leu Ser Asn Arg Ser Ile Gly Val Leu Phe Asn Ser
20 25 30

Gly Thr His Met Val Phe Pro Ala His Arg Arg His Val His Tyr Asn
35 40 45

Leu Thr Asn Ser Arg His Phe Val Pro Thr Ser Thr Val Pro Glu Gln
50 55 60

Leu Gln Gly Gln Met Ser Ile Leu Gln Tyr Phe Ala Thr Tyr Met Glu
65 70 75 80

Lys Asn Leu Met Lys Gly Gly Asp Leu Pro Cys His Glu Glu Gly Ser
85 90 95

Gln Ala Pro Leu Leu Leu Leu Gln Trp Val Lys Thr Glu His Ala Leu
100 105 110

Leu Met Leu Phe Ser Asn Gly Thr Leu Gln Val Asn Phe Tyr Asn Asp
115 120 125

His Thr Lys Ile Ile Leu Cys Lys Pro Gln Asp Ala Tyr Leu Leu Thr
130 135 140

Tyr Ile Asn Arg Asp Arg Asn Ser Gln Thr Phe Leu Leu Ser Thr Leu
145 150 155 160

Ala Gln Thr Gly Cys Asn Ser Glu Met Tyr His Arg Leu Lys Tyr Thr
165 170 175

Val Lys Leu Leu Gln Gln Lys Ala Glu Ser
180 185

<210> 98

<211> 194

<212> PRT

<213> Schizosaccharomyces pombe

<400> 98

Pro Val Leu Phe Ile Thr Lys Trp Val Asp Tyr Ser Asn Lys Tyr Gly
1 5 10 15

Leu Gly Tyr Gln Leu Ser Asp Glu Ser Val Gly Val His Phe Asn Asp
20 25 30

Asp Thr Ser Leu Leu Phe Ser Ala Asp Glu Glu Val Val Glu Tyr Ala
35 40 45

Leu His Pro Lys Asp Thr Glu Ile Lys Pro Tyr Ile Tyr Pro Ala Ser
50 55 60

Lys Val Pro Glu Ser Ile Arg Ser Lys Leu Gln Leu Leu Lys His Phe
65 70 75 80

Lys Ser Tyr Met Gly Gln Asn Leu Ser Lys Ala Val Gln Asp Glu Ser
85 90 95

Phe Glu Lys Pro Lys Asn Ser Thr Ser Asn Thr Met Leu Phe Met Gln
100 105 110

His Tyr Leu Arg Thr Arg Gln Ala Ile Met Phe Arg Leu Ser Asn Gly
115 120 125

Ile Phe Gln Phe Asn Glu Leu Asp His Arg Lys Val Val Ile Ser Ser
130 135 140

Thr Ala Arg Lys Ile Ile Val Leu Asp Lys Glu Arg Glu Arg Val Glu
145 150 155 160

Leu Pro Leu Gln Glu Ala Ser Ala Phe Ser Glu Asp Leu Arg Ser Arg
165 170 175

Leu Lys Tyr Ile Arg Glu Thr Leu Glu Ser Trp Ala Ser Lys Met Glu
180 185 190

Val Ser

<210> 99
<211> 196
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 99

His Pro Met Ile Val Thr Lys Trp Val Asp Tyr Ser Asn Lys His Gly
1 5 10 15

Phe Ser Tyr Gln Leu Ser Thr Glu Asp Ile Gly Val Leu Phe Asn Asn
20 25 30

Gly Thr Thr Val Leu Arg Leu Ala Asp Ala Glu Glu Phe Trp Tyr Ile
35 40 45

Ser Tyr Asp Asp Arg Glu Gly Trp Val Ala Ser His Tyr Leu Leu Ser
50 55 60

Glu Lys Pro Arg Glu Leu Ser Arg His Leu Glu Val Val Asp Phe Phe
65 70 75 80

Ala Lys Tyr Met Lys Ala Asn Leu Ser Arg Val Ser Thr Phe Gly Arg
85 90 95

Glu Glu Tyr His Lys Asp Asp Val Phe Leu Arg Arg Tyr Thr Arg Tyr
 100 105 110

Lys Pro Phe Val Met Phe Glu Leu Ser Asp Gly Thr Phe Gln Phe Asn
 115 120 125

Phe Lys Asp His His Lys Met Ala Ile Ser Asp Gly Gly Lys Leu Val
 130 135 140

Thr Tyr Ile Ser Pro Ser His Glu Ser Thr Thr Tyr Pro Leu Val Glu
 145 150 155 160

Val Leu Lys Tyr Gly Glu Ile Pro Gly Tyr Pro Glu Ser Asn Phe Arg
 165 170 175

Glu Lys Leu Thr Leu Ile Lys Glu Gly Leu Lys Gln Lys Ser Thr Ile
 180 185 190

Val Thr Val Asp
 195

<210> 100
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 100

Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys Tyr Gly
 1 5 10 15

Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe Asn Asp
 20 25 30

Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln Tyr Ile
 35 40 45

Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His Pro Asn
 50 55 60

Ser Leu Met Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn Tyr Met
 65 70 75 80

Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg Glu Gly
85 90 95

Asp Glu Leu

<210> 101
<211> 98
<212> PRT
<213> Homo sapiens

<400> 101

Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg Thr Arg Ser Ala Ile
1 5 10 15

Ile Leu His Leu Ser Asn Gly Ser Val Gln Ile Asn Phe Phe Gln Asp
20 25 30

His Thr Lys Leu Ile Leu Cys Pro Leu Met Ala Ala Val Thr Tyr Ile
35 40 45

Asp Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser Leu Leu Glu Glu
50 55 60

Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr Ala Arg Thr
65 70 75 80

Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser Asn Arg Leu Lys
85 90 95

Ala Ser

<210> 102
<211> 87
<212> PRT
<213> Mus musculus

<400> 102

Ser Ala Gln Leu Leu Lys Ser Val Phe Val Lys Asn Val Gly Trp Ala
1 5 10 15

Thr Gln Leu Thr Ser Gly Ala Val Trp Val Gln Phe Asn Asp Gly Ser
20 25 30

Gln Leu Val Val Gln Ala Gly Val Ser Ser Ile Ser Tyr Thr Ser Pro
 35 40 45

Asp Gly Gln Thr Thr Arg Tyr Gly Glu Asn Glu Lys Leu Pro Glu Tyr
 50 55 60

Ile Lys Gln Lys Leu Gln Cys Leu Ser Ser Ile Leu Leu Met Phe Ser
 65 70 75 80

Asn Pro Thr Pro Asn Phe Gln
 85

<210> 103
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
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 <222> (1)..(1)
 <223> Xaa = Met, Tyr, His, Phe, Lys, Ile, or Leu

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa = Ala, His, Met, Thr, Phe, or Gln

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = Ser, Ala or Gly

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa = Phosphorylated Ser or phosphorylated Thr

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Xaa = Pro, Met or any amino acid except Cys

<400> 103

Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(1)
<223> Xaa = Pro or Phe

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Met, Phe, Pro, Leu, or Ile

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Met, Tyr, His, Phe, Lys, or Leu

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Ala, His, Met, Thr, Phe, or Gln

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = Ser or Ala

<220>
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<222> (6)..(6)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Pro or Met

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe, Ile, Lys, Leu, or Val

<400> 104

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa
1 5

<210> 105
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(1)
<223> Xaa = Pro, Phe, or Ile

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Phe, Ile, Met, Leu, Pro, or Val

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Gln, Met, His, Phe, Ile, or Thr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Thr, His, or Gln

<220>
<221> MOD_RES
<222> (6)..(6)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe, Leu, Ile, Val, or Lys

<400> 105

Xaa Xaa Xaa Xaa Ser Thr Pro Xaa
1 5

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Ile, Leu, Val, Phe, or Pro

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = Met, Leu, Phe, Ala, or Ile

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa = Thr or His

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> PHOSPHORYLATION

<220>
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 <222> (7)..(7)
 <223> Xaa = Pro, Asp, or Glu

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Xaa = Lys, Val, or Phe

<400> 106

Pro Xaa Xaa Xaa Ser Thr Xaa Xaa
 1 5

<210> 107
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
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 <222> (1)..(1)
 <223> Xaa = Pro or Phe

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa =Phe, Ile, Leu, Met, or Pro

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = Phe, Leu, or Met

<220>
 <221> MISC_FEATURE

<222> (4)..(4)
<223> Xaa = Thr, His, or Gln

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<222> (6)..(6)
<223> PHOSPHORYLATION

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<222> (8)..(8)
<223> Xaa = Lys, Ile, Leu, or Val

<400> 107

Xaa Xaa Xaa Xaa Ser Thr Pro Xaa
1 5

<210> 108
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(1)
<223> Xaa = Pro or Phe

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Phe, Ile, Leu, Met, or Val

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Ala, Met, Phe, Val, or Ile

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Thr, Ala, Gln, Met, or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Leu, Ile, or any amino acid other than Cys

<400> 108

Xaa Xaa Xaa Xaa Ser Thr Pro Xaa
1 5

<210> 109

<211> 222

<212> PRT

<213> Homo sapiens

<400> 109

Ala Leu Ser Asp Met Leu Gln Gln Leu His Ser Val Asn Ala Ser Lys
1 5 10 15

Pro Ser Glu Arg Gly Leu Val Arg Gln Ala Glu Ala Glu Asp Pro Ala
20 25 30

Cys Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp Tyr Ser Asp Lys
35 40 45

Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val Gly Val Leu Phe
50 55 60

Asn Asn Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly Asp Ser Leu Gln
65 70 75 80

Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr Val Ser Ser His
85 90 95

Pro Asn Ala Leu Met Lys Lys Ile Thr Leu Leu Lys Tyr Phe Arg Asn
100 105 110

Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn Ile Thr Pro Arg
115 120 125

Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg Thr Trp Phe Arg
130 135 140

Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly Ser Val Gln Ile
145 150 155 160

Asn Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys Pro Leu Met Ala
165 170 175

Ala Val Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg Thr Tyr Arg Leu
180 185 190

Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu
195 200 205

Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser Ser Ala
210 215 220

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(1)
<223> Xaa =any amino acid except Cys

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Gly, Asp, or Glu

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Leu, Ile, Met, or Val

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = Phosphorylated Ser or Phosphorylated Tyr

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Val or Ile

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe, Leu, or Ile

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = Ile, Phe, Leu, Val, or Tyr

<400> 110

Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Pro Xaa
1 5 10

<210> 111

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<220>

<221> MISC_FEATURE

<222> (1)..(2)

<223> Xaa = any amino acid except Cys

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa = Ile, Met, Val, or Leu

<220>

<221> MOD_RES

<222> (5)..(5)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa = Phe, Ile, Gln, or Tyr

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa = Val or Thr

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa = any amino acid except Cys

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa = Ile, Phe, Met, or Leu

<400> 111

Xaa Xaa Glu Xaa Ser Xaa Xaa Phe Xaa Xaa
1 5 10

<210> 112

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Asp or Glu

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Leu, Ile, or Met

<220>
<221> MOD_RES
<222> (5)..(5)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Gln, Ile, or Pro

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Val or Ile

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe, Ile, Val, Leu, or Tyr

<400> 112

Gly Tyr Xaa Xaa Ser Xaa Xaa Xaa Phe Tyr
1 5 10

<210> 113
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> Xaa = any amino acid except Cys

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa = Ile, Leu, or Trp

<220>
 <221> MOD_RES
 <222> (5)..(5)
 <223> PHOSPHORYLATION

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Xaa = Gln, Phe, or Ile

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Xaa = Ile, Leu, or Val

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Xaa = Phe, Tyr, or Pro

<400> 113

Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Tyr	Xaa	Xaa	Ala
1				5					10

<210> 114
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
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 <222> (1)..(1)
 <223> Xaa = any amino acid except Cys

<220>
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 <222> (2)..(2)
 <223> Xaa = Phe or Tyr

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = Asp or Glu

<220>


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<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Ile, Val, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = phosphorylated Ser or phosphorylated Thr

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Val, Thr, Ile, or Ser

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe or Tyr

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa = Val or Pro

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = Phe or Gly

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<400> 114

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Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
1              5              10

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<210> 115
<211> 10
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic

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<220>
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<222> (1)..(1)
<223> Xaa = any amino acid except Cys

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<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Arg or Tyr

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<220>
<221> MISC_FEATURE
<222> (3)..(3)

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<223> Xaa = Glu or Asp

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Val, Ile, or Met

<220>
<221> MOD_RES
<222> (5)..(5)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Phe, Tyr, Ile, or Gln

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Thr or Val

<220>
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<222> (9)..(9)
<223> Xaa = any amino acid except Cys

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = Phe, Met, or Tyr

<400> 115

Xaa Xaa Xaa Xaa Ser Xaa Xaa Phe Xaa Xaa
1          5          10

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(2)
<223> Xaa = any amino acid except Cys

<220>
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<222> (4)..(4)
<223> Xaa = any amino acid except Cys

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<220>
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<222> (5)..(5)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
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<222> (7)..(7)
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<223> Xaa = Phe or Tyr

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<222> (10)..(10)
<223> Xaa = any amino acid except Cys

<400> 116

Xaa Xaa Tyr Xaa Ser Xaa Xaa Xaa Ile Xaa
1          5          10

<210> 117
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(1)
<223> Xaa = any amino acid except Cys

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Asp or Glu

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Ile or Leu

<220>
<221> MOD_RES

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<222> (5)..(5)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Gln, Glu, or Phe

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Asp, Tyr, or Ile

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Phe or Tyr

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa = Asp or Pro

<400> 117

Xaa Glu Xaa Xaa Thr Xaa Xaa Xaa Xaa Ala
1 5 10

<210> 118
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
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<222> (1)..(3)
<223> Xaa is any amino acid except Cys

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Ala, Ile, Leu, Met, Asn, Pro, Ser, Thr, or Val

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is phosphorylated Ser or phosphorylated Thr

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is a biased mixture of 25% E, 75% of any amino acid except

Arg, Cys, Lys, or His

<220>
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 <222> (8)..(10)
 <223> Xaa is any amino acid except Cys

<400> 118

Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10

<210> 119
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa = Cys, Phe, Trp, or Tyr

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> Xaa = Ile, Leu, or Val

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa = any amino acid with aliphatic or aromatic side chains

<220>
 <221> MOD_RES
 <222> (5)..(5)
 <223> PHOSPHORYLATION

<220>
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 <222> (7)..(7)
 <223> Xaa = Asp, Glu, Met, or Asn

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Xaa = Phe or Ile

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Xaa = Gly, His, Lys, or Pro

<220>
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 <222> (10)..(10)
 <223> Xaa = Phe, Lys, Trp, or Tyr

<400> 119

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1				5					10

<210> 120
 <211> 10
 <212> PRT
 <213> Artificial Sequence

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 <222> (1)..(1)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa = Phe, Trp, or Tyr

<220>
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 <222> (3)..(3)
 <223> Xaa = Ile, Leu, or Val

<220>
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 <222> (4)..(4)
 <223> Xaa = any amino acid with an aliphatic or aromatic side chain

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 <223> PHOSPHORYLATION

<220>
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 <222> (7)..(7)
 <223> Xaa = Ala, Met, Asn, Pro, or Gln

<220>
 <221> MISC_FEATURE

<222> (8)..(8)
 <223> Xaa = Cys or Phe

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 <222> (9)..(9)
 <223> Xaa = Asp, Glu, Gly, Lys, or Pro

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 <222> (10)..(10)
 <223> Xaa = Phe, Gly, His, or Lys

 <400> 120

Xaa	Xaa	Xaa	Xaa	Thr	Gln	Xaa	Xaa	Xaa	Xaa
1				5					10

<210> 121
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (1)..(4)
 <223> Xaa = any amino acid

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 <222> (6)..(7)
 <223> Xaa = any amino acid

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 <222> (8)..(8)
 <223> Xaa = Phe, Ile, Leu, Asn, or Tyr

<220>
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 <222> (9)..(10)
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<400> 121

Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10

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 <222> (1)..(4)
 <223> Xaa = any amino acid

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<220>
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 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Xaa = Phe or Tyr

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Xaa = Phe, Ile, Leu, Val, Trp, or Tyr

<220>
 <221> MISC_FEATURE
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 <223> Xaa = any amino acid

<400> 122

Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 123
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 <212> PRT
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<220>
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<220>

<221> MOD_RES
<222> (7)..(7)
<223> PHOSPHORYLATION

<400> 123

Gly Ala Ala Tyr Asp Ile Ser Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 124
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> PHOSPHORYLATION

<400> 124

Gly Ala Ala Tyr Asp Ile Thr Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 125
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 125

Gly Ala Ala Tyr Asp Ile Ser Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 126
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 126

Gly Ala Ala Tyr Asp Ile Thr Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 127
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<400> 127

Gly Ala Ala Tyr Asp Ile Ser Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 128
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<220>
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Gly Ala Ala Tyr Asp Ile Ser Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15

<210> 129
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<220>
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<400> 129

Gly Ala Ala Tyr Asp Ile Thr Gln Val Phe Pro Phe Ala Lys Lys Lys
1 5 10 15